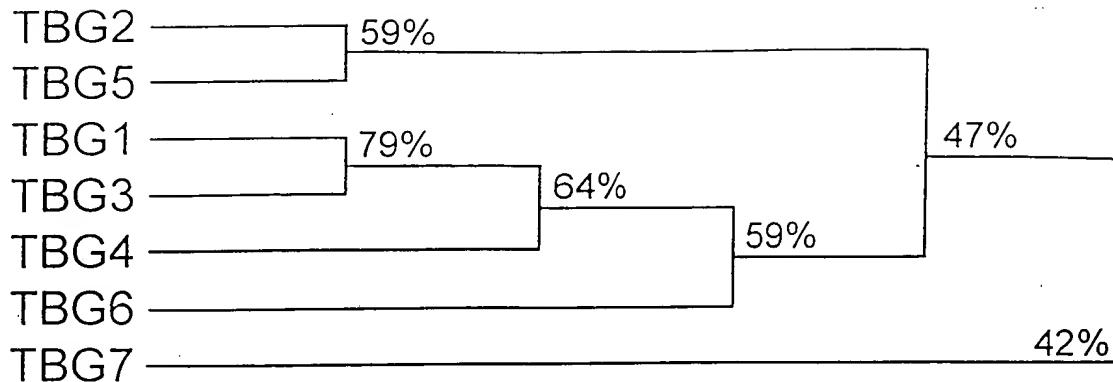




A



B

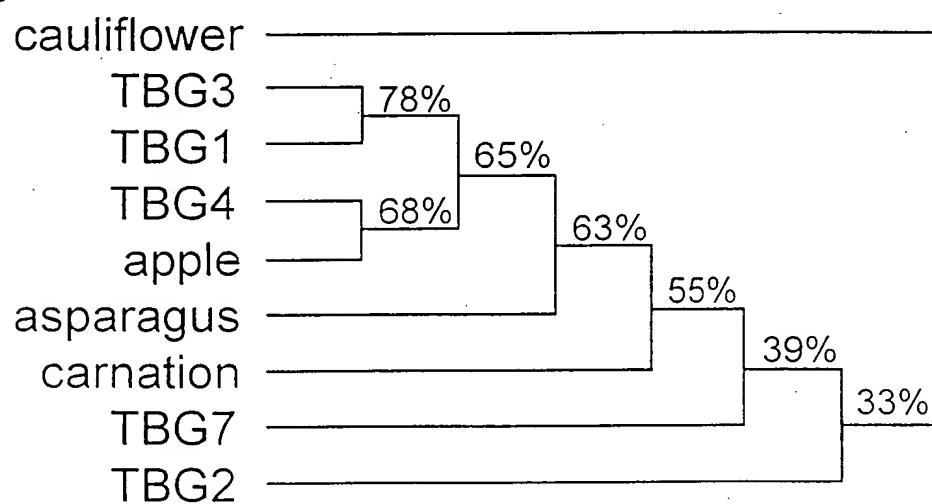
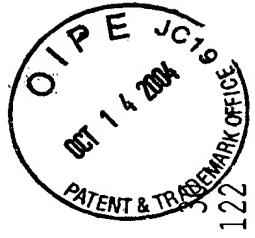


Figure 1. β -Galactosidase phylogenetic tree based on shared amino acid sequence identity. A. Tomato β -galactosidase (TBG) cDNAs. B. Plant β -galactosidases. Higgins-Sharp algorithm (UPGMA method)

FIG. I



TTTTTCTTGTCTTTCAGCACTAG
 31 AGCCTAGAAGGAAAAAGAAAGTATGGACTAATGGATAACATAAAACATAAAAGAGAGAAA
 123 AAAACAGCTGTTCCCTCACTACTTTTCCCAATCTATATAATTGCAAGAACTTGAATTAAAA
 215 GAATAATAAGCTGTGGGGTAGGAGAAGTTAGTTCATTAAGGCACAATCTTGATTGTTGACAAAT

 306 ATG GGT TTT TGG ATG ATG GCA ATG TTG CTG ATG TTG TTA TTG TGT TCA TGG GTT TCT TGT GGA ATT GCT TCT
 1 Met Gly Phe Trp Met Ala Met Leu Met Leu Leu Cys Leu Trp Val Ser Cys Gly Ile Ala Ser 23

 375 GTT TCA TAT GAC CAT AAA GCT ATC ATT GTA AAT GGA CAA AGA AAA ATT CTC ATT TCT GGA TCC ATT CAC
 24 Val Ser Tyr Asp His Lys Ala Ile Ile Val Asn Gly Gln Arg Lys Ile Leu Ile Ser Gly Ser Ile His 46

 444 TAC CCT AGA AGC ACC CCT GAG ATG TGG CCA GAT CTT ATT CAG AAG GCA AAA GAA GGG GGA GTT GAT GTT
 47 Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Glu Gly Val Asp Val 69

 513 ATA CAG ACT TAT GTT TTC TGG AAT GGG CAT GAG CCT GAA GAA AAA TAT TAT TAT GAA GAG AGG TAT
 70 Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Glu Glu Gly Lys Tyr Tyr Phe Glu Glu Arg Tyr 92

 582 GAT TTA GTG AAG TTC ATT AAA GTG GTG CAA GAA GCA GGA CTT TAT GTG CAT CTT AGG ATT GGA CCT TAT
 93 Asp Leu Val Lys Phe Ile Lys Val Val Gly Leu Gly Leu Val His Leu Arg Ile Gly Pro Tyr 115

 651 GCA TGT GCT GAA TGG AAT TTT GGG GGT TTT CCT GTT TGG CTG AAG TAT GTT CCA GGT ATT AGT TTC AGA
 116 Ala Cys Ala Glu Trp Asn Phe Gly Gly Phe Pro Val Trp Leu Lys Tyr Val Pro Gly Ile Ser Phe Arg 138

 720 ACA AAC AAT GAG CCA TTC AAG GCT GCA AAG TTC ACT ACT AAG ATT GTT GAT ATG ATG AAA GCA
 139 Thr Asn Asn Glu Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Thr Lys Ile Val Asp Met Met Lys Ala 161

 789 GAA AAG CTC TAT GAA ACT CAG GGT GGT CCA ATT ATT CTA TCT CAG ATA GAA AAT GAA TAT GGA CCT ATG
 162 Glu Lys Leu Tyr Glu Thr Gln Gly Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr Gly Pro Met 184

FIG. 2A-1

858	GAG	TGG	GAA	CTA	GGT	GAA	CCT	GGT	AAA	GTT	TAC	TCA	GAA	TGG	GCA	GCC	AAA	ATG	GCT	GTG	GAT	CTT	GGC			
185	Glu	Trp	Glu	Leu	Gly	Glu	Pro	Gly	Lys	Val	Tyr	Ser	Glu	Trp	Ala	Ala	Val	Asp	Leu	Gly			926			
927	ACT	GGT	GTC	CCA	TGG	ATC	ATG	TGC	AAG	CAA	GAT	GAT	GTC	CCT	GAT	CCT	ATT	AAT	ACT	TGC	AAT	GGT		995		
208	Thr	Gly	Val	Pro	Trp	Ile	Met	Cys	Lys	Gln	Asp	Asp	Val	Pro	Asp	Pro	Ile	Ile	Asn	Thr	Cys	Asn	Gly	230		
996	TTC	TAC	TGT	GAC	TAC	TTC	ACA	CCA	AAT	AAG	GCT	AAT	AAA	CCC	AAG	ATG	TGG	ACT	GAA	GCC	TGG	ACA	GCC	1064		
231	Phe	Tyr	Cys	Asp	Tyr	Phe	Thr	Pro	Asn	Lys	Ala	Asn	Lys	Pro	Lys	Met	Trp	Thr	Glu	Ala	Trp	Thr	Ala	253		
1065	TGG	TTT	ACC	GAA	TTT	GGG	GGT	CCA	GTT	CCT	TAC	CGT	CCT	GCA	GAG	GAT	ATG	GCA	TTT	GCT	GTC	GCA	AGA	1133		
254	Trp	Phe	Thr	Glu	Phe	Gly	Gly	Pro	Val	Pro	Val	Pro	Tyr	Arg	Pro	Ala	Glu	Asp	Met	Ala	Phe	Ala	Val	Ala	Arg	276
1134	TTT	ATA	CAA	ACG	GGG	GGC	TCC	TTC	ATC	AAT	TAC	TAT	ATG	TAT	CAT	GGA	GGA	ACA	AAC	TTT	GGA	AGG	ACT		1202	
277	Phe	Ile	Gln	Thr	Gly	Gly	Ser	Phe	Ile	Asn	Tyr	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	299	
1203	TCT	GGT	GGC	CCA	TTT	ATT	GCT	ACT	AGT	TAT	GAT	TAT	GAT	GCA	CCC	CTA	GAT	GAA	TTT	GGG	TCA	TTA	CGG	1271		
300	Ser	Gly	Gly	Pro	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Pro	Gly	Ser	Leu	Arg	322		
1272	CAG	CCT	AAA	TGG	GGT	CAT	CTG	AAA	GAT	CTA	CAT	AGA	GCA	ATA	AAG	CTC	TGT	GAG	CCA	GCT	TTA	GTA	TCT	1340		
323	Gln	Pro	Lys	Trp	Gly	His	Leu	Lys	Asp	Leu	His	Arg	Ala	Ile	Lys	Leu	Cys	Glu	Pro	Ala	Leu	Val	Ser	345		
1341	GTA	GAT	CCA	ACT	GTG	ACA	TCC	TTA	GGA	AAC	TAT	CAA	GAG	GCA	CGT	GTT	TTC	AAG	TCA	GAG	TCT	GGG	GCC	1409		
346	Val	Asp	Pro	Thr	Val	Thr	Ser	Leu	Gly	Asn	Tyr	Gln	Glu	Ala	Arg	Val	Phe	Lys	Ser	Glu	Ser	Gly	Ala	368		
1410	TGC	GCT	GCC	TTC	CTA	GCA	AAT	TAC	AAC	CAG	CAC	TCT	TTT	GCT	AAA	GTG	GCA	TTT	GGG	AAC	ATG	CAT	TAT	1478		
369	Cys	Ala	Ala	Phe	Leu	Ala	Asn	Tyr	Asn	Gln	His	Ser	Phe	Ala	Lys	Val	Ala	Phe	Gly	Asn	Met	His	Tyr	391		

FIG. 2A-2

1479	AAC	TTG	CCA	CCC	TGG	TCT	ATC	AGC	ATT	CTT	CCC	GAC	TGC	AAG	AAC	ACT	GTC	TAT	AAT	ACT	GCA	AGG	GTT	1547	
392	Asn	Leu	Pro	Pro	Trp	Ser	Ile	Ser	Ile	Leu	Pro	Asp	Cys	Lys	Asn	Thr	Val	Try	Asn	Thr	Ala	Arg	Val	414	
1548	GGT	GCT	CAA	AGT	GCT	CAG	ATG	AAG	ATG	ACT	CCA	GTC	AGT	AGA	GGA	TTC	TCA	TGG	GAG	TCA	TTC	AAT	GAA	1616	
415	Gly	Ala	Gln	Ser	Ala	Gln	Met	Lys	Met	Thr	Pro	Val	Ser	Arg	Gly	Phe	Ser	Trp	Glu	Ser	Trp	Glu	Asn	Glu	437
1617	GAC	GCA	GCA	TCG	CAT	GAA	GAC	GAC	ACT	TTC	ACA	GTT	GTT	GGG	TTA	TG	GAG	CAG	ATT	AAT	ATC	ACA	AGA	1685	
438	Asp	Ala	Ala	Ser	His	Glu	Asp	Asp	Thr	Phe	Thr	Val	Val	Gly	Leu	Leu	Glu	Gln	Ile	Asn	Ile	Thr	Arg	460	
1686	GAT	GTA	TCT	GAT	TAC	TTC	TGG	TAT	ATG	ACT	GAC	ATT	GAG	ATT	GAT	CCA	ACA	GAA	GGA	TTT	TTG	AAT	AGT	1754	
461	Asp	Val	Ser	Asp	Tyr	Ieu	Trp	Tyr	Met	Thr	Asp	Ile	Glu	Ile	Asp	Pro	Thr	Glu	Gly	Phe	Leu	Asn	Ser	483	
1755	GGA	AAT	TGG	CCT	TGG	CTT	ACT	GTC	TTT	TCT	GCT	GGC	CAT	GCA	TTG	CAT	GTA	TTC	GTC	AAT	GGT	CAA	TTA	1823	
484	Gly	Asn	Trp	Pro	Trp	Ieu	Thr	Val	Thr	Val	Gly	Ser	Ala	Gly	His	Ala	Leu	His	Val	Phe	Val	Asn	Gly	Leu	506
1824	GCA	GGG	ACT	GTG	TAC	GGG	AGT	TTA	GAA	AAC	CCA	AAA	CTA	ACT	TTC	AGC	AAC	GGT	ATA	AAT	CTG	AGA	GCT	1892	
507	Ala	Gly	Thr	Val	Tyr	Gly	Ser	Leu	Glu	Asn	Pro	Lys	Leu	Thr	Phe	Ser	Asn	Gly	Ile	Asn	Ile	Arg	Ala	529	
1893	GGT	GTG	AAC	AAG	ATT	TCT	CTG	CTA	AGC	ATT	GCT	GTT	GGT	CTT	CCG	AAC	GTC	CTT	GAG	ACA	1961				
530	Gly	Val	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Val	Gly	Pro	His	Phe	Glu	Thr	552	
1962	TGG	AAT	GCT	GGT	GTT	CTT	GGA	CCA	GTT	TCA	CTT	AAT	GGA	CTT	AAT	GAA	GGA	ACA	AGA	GAT	TTA	ACA	TGG	2030	
553	Trp	Asn	Ala	Gly	Val	Ieu	Gly	Pro	Val	Ser	Ieu	Asn	Gly	Leu	Asn	Glu	Gly	Thr	Arg	Asp	Leu	Thr	Trp	575	
2031	CAG	AAA	TGG	TTC	TAC	AAG	GGT	CTA	AAA	GGA	GAA	GCC	CTG	AGT	CTT	CAT	TCA	CTC	AGT	GGT	AGC	CCA	2099		
576	Gln	Lys	Trp	Phe	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Ieu	His	Ser	Leu	Ser	Gly	Ser	Pro	598	

FIG. 2A-3

FIG. 2A-4

2100	TCC	GTG	GAG	TGG	GTG	GAA	GGC	TCT	TTA	GTG	GCT	CAG	AAG	CAG	CCA	CTC	AGT	TGG	TAT	AAG	ACT	ACA	TTC			
599	Ser	Val	Glu	Trp	Val	Glu	Gly	Ser	Leu	Val	Ala	Gln	Pro	Leu	Ser	Trp	Tyr	Lys	Thr	Thr	Thr	Asn	621			
2169	AAT	GCT	CCA	GAT	GGG	AAT	GAA	CCT	TG	GCT	TTA	GAT	ATG	AAA	ACC	ATG	GGC	AAA	GGT	CAA	GTA	TGG	ATA	2237		
622	Asn	Ala	Pro	Asp	Gly	Asn	Glu	Pro	Leu	Ala	Leu	Asp	Met	Asn	Thr	Met	Gly	Lys	Gly	Gln	Val	Trp	Ile	644		
2238	AAT	GGT	CAG	AGC	CTC	GGG	CAC	TGG	CCT	GCA	TAT	AAA	TCA	TCT	GGA	AGT	TGT	TGT	AAC	TAT	2306					
645	Asn	Gly	Gln	Ser	Leu	Gly	Arg	His	Trp	Pro	Ala	Tyr	Lys	Ser	Ser	Gly	Ser	Cys	Ser	Val	Cys	Asn	Tyr	667		
2307	ACT	GGC	TGG	TIT	GAT	GAG	AAA	AAG	TGC	CTA	ACT	AAC	TGT	GGT	GAG	GGC	TCA	CAA	AGA	TGG	TAC	CAC	GTA	2375		
668	Thr	Gly	Trp	Phe	Asp	Glu	Lys	Lys	Cys	Leu	Thr	Asn	Cys	Gly	Glu	Gly	Ser	Gln	Arg	Trp	Tyr	His	Val	690		
2376	CCC	CGG	TCT	TGG	CTG	TAT	CCT	ACT	GGG	AAT	TTG	TTA	GTT	GTA	TTC	GAG	GAA	TGG	GG	TAC	CAC	GTA	2444			
691	Pro	Arg	Ser	Trp	Leu	Tyr	Pro	Thr	Gly	Asn	Leu	Leu	Val	Val	Val	Phe	Glu	Glu	Glu	Trp	Gly	Gly	Asp	Pro	Tyr	713
2445	GGA	ATC	ACT	TTA	GTC	AAA	AGA	GAA	ATA	GGG	AGT	GTT	TGT	GCT	GAG	GAA	TGG	GG	GAT	CCT	TAT	2513				
714	Gly	Ile	Thr	Leu	Val	Lys	Arg	Glu	Ile	Gly	Ser	Val	Cys	Ala	Asp	Ile	Tyr	Glu	Trp	Gly	Gly	Asp	Pro	Tyr	736	
2514	TTG	AAT	TGG	CAG	AGG	CTA	GTA	TCT	GGT	AAG	TTT	GAC	AGA	CCT	CTC	AGA	CCT	AAA	GCC	CAT	CTT	AAG	TGT	2582		
737	Ieu	Asn	Trp	Gln	Arg	Leu	Val	Ser	Gly	Lys	Phe	Asp	Arg	Pro	Leu	Arg	Pro	Lys	Ala	His	Leu	Lys	Cys	759		
2583	GCA	CCT	GGT	CAG	AAG	ATT	TCT	TCA	ATC	AAA	TTT	GCA	AGC	TTT	GGA	ACA	CCA	GAG	GGA	GTT	TGT	GGG	AAC	2651		
760	Ala	Pro	Gly	Gln	Lys	Ile	Ser	Ser	Ile	Lys	Phe	Ala	Ser	Phe	Gly	Thr	Pro	Glu	Gly	Val	Cys	Gly	Asn	782		
2652	TTC	CAG	CAG	GGG	AGC	TGC	CAT	GCT	CCG	CGC	TCA	TAT	GAT	GCT	TTC	AAA	AAG	AAT	TGT	GTT	GGG	AAA	GAG	2720		
783	Phe	Gln	Gln	Gly	Ser	Cys	His	Ala	Pro	Arg	Ser	Tyr	Asp	Ala	Phe	Lys	Lys	Asn	Cys	Val	Gly	Lys	Glu	805		

FIG. 2A-5

2721	TCT	TGC	TCA	GTA	CAG	ACA	CCA	GAG	AAT	TTT	GGA	GGT	GAT	CCA	TGT	CGA	AAC	GTT	CTA	AAG	AAA	CTC	
806	Ser	Cys	Ser	Val	Gln	Val	Thr	Pro	Glu	Asn	Phe	Gly	Gly	Asp	Pro	Cys	Arg	Asn	Val	Leu	Lys	Leu	828
2790	TCA	GTG	GAA	GCC	ATT	TGT	AGT	TGA	TGATTCTGAGTATAACAAGTGAAAGAACCTCATATAAACATTTCACACG	2873													
829	Ser	Val	Glu	Ala	Ile	Cys	Ser	***	836														
2874	AGCTACTAGACATCCATTAAACCCACACTACCATTGGCTTTGGCTGGTTGAAGTTGACAGTAAGCAACACACCTCTTTGATCAAAG	2965																					
2966	CTCACCTGAAATTATGAAAGATGATTGACGAAGATCTGTACATGTAAAGGTTCTGCTAATTACACATACAGATATGATTCTGATGAATCGAT	3057																					
3058	GTGCAAATTGGTTGTGTTAGGGTAGGGTAGAGAGCTGAAAGCATTGCTTCAATTGATGTTCTACATTATAACATTAATGTAAGTAAGC	3149																					
3150	AAGCAATAATTCAATTGCTTGCACATGAAAMGCATTACTATGTTGCAGTACAAAAAA	3224																					

1	2
3 AGC AGA AGA AAA ACA CTG AAT TTT CCG TTA ATA CTA ACG GTG TTA ACT ATC CAC TTT GTG ATC GTC GCC	71
1 Ser Arg Arg Lys Thr Leu Asn Phe Pro Leu Ile Leu Thr Val Ile His Phe Val Ile Val Ala	23
72 GGC GAG TAT TTC AAG CCG TTC AAT GTC ACC TAC GAT AAC CGA GCT CTC ATC GGC GGT AAA CGC CGT	140
24 GLY Glu Tyr Phe Lys Pro Phe Asn Val Thr Tyr Asp Asn Arg Ala Leu Ile Gly Gly Lys Arg Arg	46
141 ATG CTT ATC TCC GCC GGA ATT CAC TAC CCT CGC GCC ACT CCT GAG ATG TGG CCC ACA TTG ATA GCT AGG	209
47 Met Leu Ile Ser Ala Gly Ile His Tyr Pro Arg Ala Thr Pro Glu Met Trp Pro Thr Leu Ile Ala Arg	69
210 AGC AAA GAA GGT GGT GCA GAT GTC ATC GAG ACT TAT ACA TTT TGG AAT GGT CAT GAG CCA ACC AGG GGA	278
70 Ser Lys Glu Gly Ala Asp Val Ile Glu Thr Tyr Phe Trp Asn Gly His Glu Pro Thr Arg Gly	92
279 CAG TAC AAT TTT GAA GGA AGA TAT GAT ATT GTC AAG TTC GCA AAG CTA GTC GGA TCT CAT GGA CTG TTC	347
93 Gln Tyr Asn Phe Glu Gly Arg Tyr Asp Ile Val Lys Phe Ala Lys Leu Val Gly Ser His Gly Leu Phe	115

FIG. 2B-1

348	CTC	TTT	ATT	CGA	ATA	GGT	CCT	TAT	GCC	TGT	GCA	GAA	TGG	CCC	ATA	TGG	CTT	CGT	
116	Leu	Phe	Ile	Arg	Ile	Gly	Pro	Tyr	Ala	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Arg
417	GAT	ATA	CCT	GGG	ATA	GAA	TTT	CGA	ACA	GAT	AAT	GCA	CCA	TTC	AAG	GAG	ATG	GAG	
139	Asp	Ile	Pro	Gly	Ile	Glu	Phe	Arg	Thr	Asp	Asn	Ala	Pro	Phe	Lys	Glu	Glu	Met	Glu
486	AAG	ATA	GTT	GAT	CTT	ATG	ATA	TCT	GAG	TGC	CTC	TTT	TCG	TGG	CAA	GGT	CCT	ATC	
162	Lys	Ile	Val	Asp	Leu	Met	Ile	Ser	Glu	Ser	Leu	Phe	Ser	Trp	Gln	Gly	Pro	Ile	Ile
555	ATT	GAA	AAT	GAA	TAT	GGA	AAT	GTT	GAA	AGC	TCA	TTC	GGT	CCC	AAG	GAA	TTA	TAT	
185	Ile	Glu	Asn	Glu	Tyr	Gly	Asn	Val	Glu	Ser	Ser	Phe	Gly	Pro	Lys	Gly	Leu	Tyr	Met
624	GCT	GAA	ATG	GCT	GTT	GGT	CTT	GGT	GCT	GTT	CCA	TGG	GTC	ATG	TGC	AGG	CAA	ACT	
208	Ala	Glu	Met	Ala	Val	Gly	Leu	Gly	Ala	Gly	Val	Pro	Trp	Val	Met	Cys	Arg	Gln	Thr
693	TAC	ATC	ATA	GAT	ACT	TGT	AAT	GCA	TAC	TAT	TGT	GAT	GGG	TTC	ACG	CCG	AAT	TCC	
231	Tyr	Ile	Ile	Asp	Thr	Cys	Asn	Ala	Tyr	Tyr	Cys	Asp	Gly	Bhe	Thr	Pro	Asn	Ser	Glu
762	ATT	TGG	ACT	GAG	AAT	TGG	TTT	GCA	GAT	TGG	GGT	GAA	AGA	CTT	CCA	TAT	AGA	CCT	
254	Ile	Trp	Thr	Glu	Asn	Trp	Asn	Gly	Trp	Phe	Ala	Asp	Trp	Gly	Glu	Arg	Leu	Pro	Tyr
831	GAT	ATT	GCA	TTT	GCA	ATT	GCT	CGT	TTC	TTT	CAA	CGT	GGG	GGC	AGC	TTA	CAG	AAC	
277	Asp	Ile	Ala	Phe	Ala	Ile	Ala	Arg	Phe	Phe	Gln	Arg	Gly	Ser	Leu	Gln	Asn	Tyr	Tyr
900	GGT	GGG	ACA	AAT	TTT	GGC	CGG	ACT	GCT	GGT	GGC	CCA	ACT	CAA	ATC	ACT	AGC	TAT	
300	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	Ala	Gly	Pro	Thr	Gln	Ile	Thr	Ser	Tyr	Asp	Ala

FIG. 2B-2

969	CTG	GAT	GAA	TAT	GGG	CTA	CGT	CAA	CCT	AAA	TGG	GGC	CAT	TTG	AAG	GAT	CTG	CAT	GCT	GCT	ATA	AAG	1037		
323	Leu	Asp	Glu	Tyr	Gly	Leu	Leu	Arg	Gln	Pro	Lys	Trp	Gly	His	Leu	Lys	Asp	Leu	His	Ala	Ala	Ile	Lys	345	
1038	CTT	TGT	GAA	CCA	GCT	CTT	GTC	GCT	GAT	TCA	CCT	CAG	TAT	ATT	AAA	CTG	GGA	CCA	AAA	CAG	GAG	GCA	1106		
346	Leu	Cys	Glu	Pro	Ala	Leu	Val	Ala	Ala	Asp	Ser	Pro	Gln	Tyr	Ile	Lys	Leu	Gly	Pro	Lys	Gln	Glu	Ala	345	
1107	CAT	GTC	TAT	CGT	GGG	ACA	TCC	AAC	ATT	GGC	CAA	TAT	ATG	TCC	TTA	AAT	GAA	GGC	ATA	TGC	GCA	GCA	1175		
369	His	Val	Tyr	Arg	Gly	Thr	Ser	Asn	Asn	Ile	Gly	Gln	Tyr	Met	Ser	Leu	Asn	Glu	Gly	Ile	Cys	Ala	Ala	391	
1176	TTT	ATT	GCA	AAT	ATT	GAT	GAA	CAT	GAA	TCA	GCA	ACA	GTC	AAA	TTT	TAC	GGT	CAA	GAG	TTC	ACT	TTA	CCT	1244	
392	Phe	Ile	Ala	Asn	Ile	Asp	Glu	His	Glu	Ser	Ala	Thr	Val	Lys	Phe	Tyr	Gly	Gln	Glu	Gly	Phe	Thr	Leu	Pro	414
1245	CCA	TGG	TCA	GTG	GTA	TTC	TGC	CAG	ATT	GCA	GAA	ATA	CAG	CTT	TCA	ACA	CAG	CTA	AGG	TGG	GGG	CAC	AAA	1313	
415	Pro	Trp	Ser	Val	Val	Phe	Cys	Gln	Ile	Ala	Glu	Ile	Gln	Leu	Ser	Thr	Gln	Leu	Arg	Trp	Gly	His	Lys	437	
1314	CTT	CAA	TCA	AAA	CAG	TGG	GCT	CAG	ATT	CTG	TTT	CAG	TTG	GGA	ATA	ATT	CTT	TGT	TTC	TAC	AAG	TTA	TCA	1382	
438	Leu	Gln	Ser	Lys	Gln	Trp	Ala	Gln	Ile	Leu	Phe	Gln	Leu	Gly	Ile	Ile	Leu	Cys	Phe	Tyr	Lys	Leu	Ser	460	
1383	CTA	AAA	GCA	AGC	TCG	GAA	AGT	TTT	TCA	CAA	TCT	TGG	ATG	ACA	TTG	AAG	GAG	CCA	CTT	GGT	GTG	TGG	GGT	1451	
461	Leu	Lys	Ala	Ser	Ser	Glu	Ser	Phe	Ser	Gln	Ser	Trp	Met	Thr	Leu	Lys	Glu	Pro	Leu	Gly	Val	Trp	Gly	483	
1452	GAC	AAG	AAT	TTC	ACT	TCT	AAA	GGA	ATA	CTG	GAG	CAT	CTG	AAT	GTG	ACA	AAA	GAC	CAG	TCT	GAT	TAC	CTG	1520	
484	Asp	Lys	Asn	Phe	Thr	Ser	Lys	Gly	Ile	Leu	Glu	His	Leu	Asn	Val	Thr	Lys	Asp	Gln	Ser	Asp	Tyr	Leu	506	
1521	TGG	TAT	CTG	ACC	AGG	ATA	TAT	ATT	TCT	GAT	GAC	ATC	TCA	TTT	TGG	GAG	GAA	AAT	GAT	GTT	AGT	CCA	1589		
507	Trp	Tyr	Leu	Thr	Arg	Ile	Tyr	Ile	Ser	Asp	Asp	Ile	Ser	Phe	Trp	Glu	Glu	Asn	Asp	Val	Ser	Pro	529		

FIG. 2B-3

1590	ACA	ATT	GAT	ATT	GAT	AGC	ATG	CGT	GAT	TTT	GTT	CGC	ATT	TTT	GTT	AAT	GGG	CAG	CTT	GCA	GGT	AGT	GTG	
530	Thr	Ile	Asp	Ile	Asp	Ser	Met	Arg	Asp	Phe	Val	Arg	Ile	Phe	Val	Asn	Gly	Gln	Leu	Ala	Gly	Ser	Val	552
1659	AAA	GGC	AAA	TGG	ATC	AAG	GTG	GTT	CAA	CCT	GTT	AAG	CTG	GTT	CAG	GGA	TAC	AAC	GAC	ATA	CTG	CTA	TTA	1727
553	Lys	Gly	Lys	Trp	Ile	Lys	Val	Val	Gln	Pro	Val	Lys	Leu	Val	Gln	Gly	Tyr	Asn	Asp	Ile	Leu	Leu	Leu	575
1728	TCT	GAG	ACG	GTG	GGG	TTG	CAG	AAT	TAT	GGT	GCC	TTC	TTG	GAG	AAG	GAT	GGG	GCA	GGT	TTT	AAA	GGT	CAG	1796
576	Ser	Glu	Thr	Val	Gly	Leu	Gln	Asn	Tyr	Gly	Ala	Phe	Leu	Glu	Lys	Asp	Gly	Ala	Gly	Phe	Lys	Gly	Gln	598
1797	ATA	AAG	CTT	ACA	GGG	TGC	AAA	AGC	GGG	GAT	ATC	AAT	CTC	ACA	ACA	TCT	TTA	TGG	ACC	TAC	CAG	GTG	GGG	1865
599	Ile	Lys	Leu	Thr	Gly	Cys	Lys	Ser	Gly	Asp	Ile	Asn	Leu	Thr	Thr	Ser	Leu	Trp	Thr	Tyr	Gln	Val	Gly	621
1866	CTT	AGA	GGC	GAA	TTC	CTG	CTG	GAA	GTA	TAT	GTC	AAT	AGT	ACT	GAA	AGT	GCA	GGA	TGG	ACT	GAG	TTT	CCC	1934
622	Leu	Arg	Gly	Glu	Phe	Leu	Glu	Val	Tyr	Asp	Val	Asn	Ser	Thr	Glu	Ser	Ala	Gly	Trp	Thr	Glu	Phe	Pro	644
1935	ACT	GGT	ACA	ACT	CCG	TCA	GTC	TTT	TCG	TGG	TAC	AAG	ACA	AAG	TTT	GAT	GCC	CCA	GGG	ACA	GAT	CCA	2003	
645	Thr	Gly	Thr	Thr	Pro	Ser	Val	Phe	Ser	Trp	Tyr	Lys	Thr	Lys	Phe	Asp	Ala	Pro	Gly	Gly	Thr	Asp	Pro	667
2004	GTT	GCT	CTT	GAT	TTT	AGT	AGC	ATG	GGA	AAA	GGT	CAG	GCA	TGG	GTT	AAT	GGC	CAC	CAT	GTA	GGA	AGA	TAT	2072
668	Val	Ala	Leu	Asp	Phe	Ser	Ser	Met	Gly	Lys	Gly	Gln	Ala	Trp	Val	Asn	Gly	His	His	Val	Gly	Arg	Tyr	690
2073	TGG	ACT	TTG	GTT	GCA	CCA	AAT	GGA	TGT	GGA	AGA	ACT	TGT	GAT	TAT	CGT	GGT	GCT	TAC	CAC	TCT	GAT	2141	
691	Trp	Thr	Leu	Val	Ala	Pro	Asn	Asn	Gly	Cys	Gly	Arg	Thr	Cys	Asp	Tyr	Arg	Gly	Ala	Tyr	His	Ser	Asp	713
2142	AAA	TGT	AGG	ACA	AAC	TGT	GGA	GAG	ATT	ACT	CAG	GCC	TGG	TAC	CAT	ATA	CCT	AGA	TCA	TGG	CTA	AAG	ACA	2210
714	Lys	Cys	Arg	Thr	Asn	Cys	Gly	Glu	Ile	Thr	Gln	Ala	Trp	Tyr	His	Ile	Pro	Arg	Ser	Trp	Leu	Lys	Thr	736

FIG. 2B-4

2211	TAA	AAT	GTA	CTA	GTT	ATC	TTT	GAA	GCA	GAT	AAA	ACT	CCG	TTT	GAT	ATT	TCC	ATT	TCG	ACG	CGT	
737	Leu	Asn	Val	Ile	Leu	Val	Ile	Phe	Glu	Glu	Thr	Asp	Lys	Thr	Pro	Phe	Asp	Ile	Ser	Ile	Ser	Arg
2280	TCT	ACT	GAA	ACC	ATT	TGT	GCT	CAA	GTA	TCG	GAA	AAG	CAC	TAT	CCA	CCT	CTA	CAT	AAG	TGG	TCT	TCG
760	Ser	Thr	Glu	Thr	Ile	Cys	Ala	Gln	Val	Ser	Glu	Lys	His	Tyr	Pro	Pro	Leu	His	Lys	Trp	Ser	His
2349	GAG	TTT	GAC	AGA	AAG	TTG	TCT	CTG	ATG	GAT	AAA	ACA	CCA	GAA	ATG	CAC	TTG	CAG	TGT	GAC	GAA	CAT
783	Glu	Phe	Asp	Arg	Lys	Leu	Ser	Leu	Met	Asp	Lys	Thr	Pro	Glu	Met	His	Leu	Gln	Cys	Asp	Glu	Gly
2418	ACA	ATC	TCT	TCT	ATT	GAA	TTT	GCA	AGC	TAT	GGA	AGT	CCG	AAT	GGC	AGC	TGT	CAA	AAG	ITC	TCA	CAA
806	Thr	Ile	Ser	Ser	Ile	Glu	Phe	Ala	Ser	Tyr	Gly	Ser	Pro	Asn	Gly	Ser	Cys	Gln	Lys	Phe	Ser	Gln
2487	AAA	TGC	CAT	GCT	GCA	AAT	TCC	TTG	TCT	GTT	GTA	TCT	CAG	GCT	TGT	ATA	GGA	AGA	ACT	AGT	TGC	AGC
829	Lys	Cys	His	Ala	Ala	Asn	Ser	Leu	Ser	Val	Val	Ser	Gln	Ala	Cys	Ile	Gly	Arg	Thr	Ser	Cys	Ser
2555	GGC	ATT	TCC	AAT	GGT	GTA	TTT	GGA	GAT	CCA	TGT	CGA	CAC	GTT	GTG	AAG	AGT	TTG	GCT	GTT	CAA	GCA
852	Gly	Ile	Ser	Asn	Gly	Val	Phe	Gly	Asp	Pro	Cys	Arg	His	Val	Val	Lys	Ser	Leu	Ala	Val	Gln	Ala
2625	TGC	TCA	CCA	CCA	GAC	CTC	AGC	ACT	TCA	GCT	TCC	TCG	TGA	GGAGACTCTGGTAACACGTTAACCTTTAGAACGAA								
875	Cys	Ser	Pro	Pro	Pro	Asp	Leu	Ser	Thr	Ser	Ala	Ser	Ser	*	*	*	*	*	*	*	*	*
2703	ACGATCCCTAAAGTCCACTCGTTCCCCGGAGCCCTCTGCTACATTCTCAGATGGCATCGTTACAAATCAGGCCGAGAAACGTAC																					
2795	ATGGACGATTATTACTTGTTAAATATTGGTTACTGTATAATGAAAGGAAATAAATGTTGCTTATGCTGAAATTATATGACAA																					
2887	AGTAACAAATGAAAATAGAAAACCTCCGTCAAAGATTAAACACCAATTAAACATGATTAACTTAGTTAACATGATTAAAAAA																					
2979	AAAAAA																					

FIG. 2B-5

1	AAGAGGAAATAAAGTTAAGGGGGAAAAGTTTCATTTCCTTAAAGGCCAAATCTGATAGAAAAGGAGATAATTTCAC	30 121
122	ATG GGT TGT ACG CTT ATA CTA ATG TTG AAT GTG TTG GTG TTG GGT TCA TGG GTT TCT TGT GGA	190 23
1	Met GLY Cys Thr Leu Ile Leu Met Leu Asn Val Leu Val Leu Gly Ser Trp Val Phe Ser GLY	
191	ACA GCT TCT GTT TCA TAT GAC CAT AGG GCT ATT ATT GTA AAT GGA CAA AGA AGA ATA CTT ATT TCT GGT	259
24	Thr Ala Ser Val Ser Tyr Asp His Arg Ala Ile Ile Val Asn Gly Gln Arg Arg Ile Leu Ile Ser GLY	46
260	TCT GTT CAT TAT CCA AGA AGC ACT CCT GAG ATG TGG CCA GGT ATT ATT CAA AAG GCT AAA GAA GGA GGT	328
47	Ser Val His Tyr Pro Arg Ser Thr Pro Glu Met Trp Pro Gly Ile Ile Gln Lys Ala Lys Glu GLY GLY	69
329	GTC GAT GTG ATT CAG ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT CAA CAA GGG AAA TAT TAT TTT GAA	397
70	Val Asp Val Ile Gln Thr Tyr Val Phe Trp Asn Gly His Glu Pro Gln Gln GLY Lys Tyr Tyr Phe Glu	92
398	GGG AGA TAT GAT TTA GTG AAG TTT ATT AAG CTG GTG CAC CAA GCA GGA CTT TAT GTC CAT CTT AGA GTT	466
93	Gly Arg Tyr Asp Leu Val Lys Phe Ile Lys Leu Val His Gln Ala GLY Leu Tyr Val His Leu Arg Val	115
467	GGA CCT TAT GCT TGT GCT GAA TGG AAT TTT GGG GGC TTT CCT GTT TGG CTG AAA TAT GTT CCA GGT ATC	535
116	Gly Pro Tyr Ala Cys Ala Glu Trp Asn Phe GLY GLY Phe Pro Val Trp Leu Lys Tyr Val Pro GLY Ile	138
536	AGT TTC AGA ACA GAT AAT GGA CCT TTC AAG GCT GCA ATG CAA AAA TTT ACT GCC AAG ATT GTC AAT ATG	604
139	Ser Phe Arg Thr Asp Asn GLY Pro Phe Lys Ala Ala Met Gln Lys Phe Thr Ala Lys Ile Val Asn Met	161
605	ATG AAA GCG GAA CGT TTG TAT GAA ACT CAA GGG CCA ATA ATT TTA TCT CAG ATT GAG AAT GAA TAT	673
162	Met Lys Ala Glu Arg Leu Tyr Glu Thr Gln GLY GLY Pro Ile Ile Leu Ser Gln Ile Glu Asn Glu Tyr	184

FIG. 2C-1

674	GGA	CCC	ATG	GAA	TGG	GAA	CTG	GGG	GCA	CCA	GGT	AAA	TCT	TAC	GCA	CAG	TGG	GCC	GCC	AAA	ATG	GCT	GTG	
185	Gly	Pro	Met	Glu	Trp	Glu	Leu	Gly	Ala	Pro	Gly	Lys	Ser	Tyr	Ala	Gln	Trp	Ala	Ala	Lys	Met	Ala	Val	207
743	GGT	CTT	GAC	ACT	GGT	GTC	CCA	TGG	GTT	ATG	TGC	AAG	CAA	GAC	GAT	GCC	CCT	GAT	CCT	ATT	ATA	AAT	GCT	742
208	Gly	Leu	Asp	Thr	Gly	Val	Pro	Trp	Val	Met	Cys	Lys	Gln	Asp	Asp	Ala	Pro	Asp	Pro	Ile	Ile	Asn	Ala	230
812	TGC	AAT	GGC	TTC	TAC	TGT	GAC	TAC	TTT	TCT	CCA	AAC	AAG	GCT	TAT	AAA	CCA	AAG	ATA	TGG	ACT	GAA	GCC	811
231	Cys	Asn	Gly	Phe	Tyr	Cys	Asp	Phe	Ser	Pro	Asn	Lys	Ala	Tyr	Lys	Pro	Lys	Pro	Ile	Trp	Thr	Glu	Ala	253
881	TGG	ACT	GCA	TGG	TTT	ACT	GGT	TTT	GGA	AAT	CCA	GTT	CCT	TAC	CGT	CCT	GCT	GAC	GAC	TTG	GCA	TTT	TCT	880
254	Trp	Thr	Ala	Trp	Phe	Thr	Gly	Phe	Gly	Asn	Pro	Val	Pro	Tyr	Arg	Pro	Ala	Glu	Asp	Leu	Ala	Phe	Ser	276
950	GTT	GCA	AAA	TTT	ATA	CAG	AAG	GGG	GGT	TCC	TTC	ATC	AAT	TAT	TAC	ATG	TAT	CAT	GGA	GGA	ACA	AAC	TTT	949
277	Val	Ala	Lys	Phe	Ile	Gln	Lys	Gly	Gly	Ser	Phe	Ile	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	299
1019	GGA	CGG	ACT	GCT	GGT	GGT	CCA	TTT	ATT	GCT	ACT	AGT	TAT	GAC	TAT	GAT	GCA	CCA	CTT	GAT	GAA	TAT	GGA	1018
300	Gly	Arg	Thr	Ala	Gly	Gly	Pro	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr	Gly	322
1088	TTA	TTG	CGA	CAA	CCA	AAA	TGG	GGT	CAC	CTG	AAA	GAT	CTG	CAT	AGA	GCA	ATA	AAG	CTT	TGT	GAA	CCA	GCT	1156
323	Leu	Leu	Arg	Gln	Pro	Lys	Trp	Gly	His	Leu	Lys	Asp	Leu	His	Arg	Ala	Ile	Lys	Leu	Cys	Glu	Pro	Ala	345
1157	TTA	GTC	TCT	GGA	GAT	CCA	GCT	GTG	ACA	GCA	CTT	GGA	CAC	CAG	GAG	GCC	CAT	GTT	AGG	TCG	AAG		1225	
346	Leu	Vai	Ser	Gly	Asp	Pro	Ala	Val	Thr	Ala	Leu	Gly	His	Gln	Gln	Glu	Ala	His	Val	Phe	Arg	Ser	Lys	368
1226	GCT	GGC	TCT	TGT	GCT	GCA	TTC	CTT	GCT	AAC	TAC	GAC	CAA	CAC	TCT	TTT	GCT	ACT	GTG	TCA	TTT	GCA	AAC	1294
369	Ala	Gly	Ser	Cys	Ala	Ala	Phe	Leu	Ala	Asn	Tyr	Asp	Gln	His	Ser	Phe	Ala	Thr	Val	Ser	Phe	Ala	Asn	391

FIG. 2C-2

1295	AGG	CAT	TAC	AAC	TTG	CCA	TGG	TCA	ATC	AGC	ATT	CTT	CCC	GAC	TGC	AAG	AAC	ACT	GTA	TTT	AAT	ACA	
392	Arg	His	Tyr	Asn	Leu	Pro	Pro	Trp	Ser	Ile	Ser	Ile	Leu	Pro	Asp	Cys	Lys	Asn	Thr	Val	Phe	Asn	Thr
1364	GCA	CGG	ATC	GGT	GCT	CAA	AGT	GCT	CAG	ATG	AAG	ATG	ACT	CCA	GTC	AGC	AGA	GGA	TTG	CCC	TGG	CAG	TCA
415	Ala	Arg	Ile	Gly	Ala	Gln	Ser	Ala	Gln	Met	Lys	Met	Thr	Pro	Val	Ser	Arg	Gly	Leu	Pro	Trp	Gln	Ser
1433	TTC	AAT	GAA	GAG	ACA	TCA	TCT	TAT	GAA	GAC	AGT	AGT	TTT	ACA	GTT	GTT	GGG	CTA	TTG	GAA	CAG	ATA	AAT
438	Phe	Asn	Glu	Glu	Thr	Ser	Ser	Tyr	Glu	Asp	Ser	Ser	Phe	Thr	Val	Val	Gly	Leu	Leu	Glu	Gln	Ile	Asn
1502	ACA	ACA	AGA	GAC	GTG	TCT	GAT	TAT	TTC	TGG	TAT	TCA	ACA	GAT	GTC	AAG	ATT	GAT	TCA	AGA	GAA	AAG	TTT
461	Thr	Thr	Arg	Asp	Val	Ser	Asp	Tyr	Leu	Trp	Tyr	Ser	Thr	Asp	Val	Lys	Ile	Asp	Ser	Arg	Glu	Lys	Phe
1571	TTG	AGA	GGC	GGG	AAA	TGG	CCT	TGG	CTT	ACG	ATC	ATG	TCA	GCT	GGG	CAT	GCA	TTG	CAT	GTT	TTT	GTG	AAT
484	Leu	Arg	Gly	Gly	Lys	Trp	Pro	Trp	Leu	Thr	Ile	Met	Ser	Ala	Gly	His	Ala	Leu	His	Val	Phe	Val	Asn
1640	GGT	CAA	TTA	GCA	GGG	ACT	GCA	TAT	GGA	AGT	TTA	GAA	AAA	CTA	ACT	TTC	AGT	AAA	GCC	GTA	AAT	1639	
507	Gly	Gln	Leu	Ala	Gly	Thr	Ala	Tyr	Gly	Ser	Leu	Glu	Lys	Pro	Lys	Leu	Thr	Phe	Ser	Lys	Ala	Val	Asn
1709	CTG	AGA	GCA	GGT	AAC	AAG	ATT	TCT	CTA	CTG	AGC	ATT	GCT	GTT	GGC	CTT	CCG	AAT	ATC	GGC	CCA	CAT	1708
530	Leu	Arg	Ala	Gly	Val	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Ile	Ala	Val	Gly	Leu	Pro	Asn	Ile	Gly	Pro	His
1778	TTT	GAG	ACA	TGG	AAT	GCT	GGT	GTT	CTT	GGG	CCA	GTC	TCA	CTA	ACT	GGT	CTT	GAC	GAG	GGG	AAA	AGA	GAT
553	Phe	Glu	Thr	Trp	Asn	Ala	Gly	Val	Leu	Gly	Pro	Val	Ser	Leu	Thr	Gly	Leu	Asp	Glu	Gly	Lys	Arg	Asp
1847	TTA	ACA	TGG	CAG	AAA	TGG	TCT	TAC	AAG	GTT	CTA	AAA	GGA	GAA	GCC	TTG	AGC	CTC	CAT	TCA	CTC	AGT	1915
576	Leu	Thr	Trp	Gln	Lys	Trp	Ser	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ala	Leu	Ser	Leu	His	Ser	Leu	Ser
																							598

FIG. 2C-3

1916	GGT	AGC	TCG	TCA	GTT	GAG	TGG	GTC	GAG	GGT	TCT	TTA	GTG	GCT	CAG	AGA	CAG	CCA	CTC	ACA	TGG	TAC	AAG	
599	Gly	Ser	Ser	Ser	Val	Glu	Trp	Val	Glu	Gly	Ser	Leu	Val	Ala	Gln	Arg	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	621
1985	AGC	ACT	TTT	AAT	GCT	CCA	GCT	GGA	AAT	GAT	CCT	TTG	GCT	TTA	GAC	TTG	AAT	ACC	ATG	GGC	AAA	GGA	CAA	2053
622	Ser	Thr	Phe	Asn	Ala	Pro	Ala	Gly	Asn	Asp	Pro	Leu	Ala	Leu	Asp	Leu	Asn	Thr	Met	Gly	Lys	Gly	Gln	644
2054	GTG	TGG	ATA	AAT	GGT	CAA	AGC	CTC	GGA	CGC	TAT	TGG	CCT	GGA	TAT	AAA	GCA	TCT	GGT	AAC	TGC	GGT	GCC	2122
645	Val	Trp	Ile	Asn	Gly	Gln	Ser	Leu	Gly	Arg	Tyr	Trp	Pro	Gly	Tyr	Lys	Ala	Ser	Gly	Asn	Cys	Gly	Ala	667
2123	TGT	TAC	TAT	GCA	GGC	TGG	TTT	AAT	GAG	AAA	AAA	TGC	CTA	AGT	AAC	TGT	GGA	GAG	GCT	TCA	CAA	CGA	TGG	2191
668	Cys	Asn	Tyr	Ala	Gly	Trp	Phe	Asn	Glu	Lys	Lys	Cys	Leu	Ser	Asn	Cys	Gly	Glu	Ala	Ser	Gln	Arg	Trp	690
2192	TAT	CAT	GTT	CCC	CGT	TCT	TGG	CTG	TAT	CCT	ACT	GGA	AAT	TGT	TTA	GTT	CTA	TTT	GAG	GAA	TGG	GGA	GGA	2260
691	Tyr	Val	Pro	Arg	Ser	Trp	Leu	Tyr	Pro	Thr	Gly	Asn	Leu	Leu	Val	Leu	Phe	Glu	Glu	Trp	Gly	Gly	713	
2261	GAG	CCT	CAT	GGA	ATC	TCT	TTG	GTA	AAA	AGA	GAA	GTT	GCA	AGT	GTT	TGT	GCA	GAT	ATA	AAC	GAA	TGG	CAA	2329
714	Glu	Pro	His	Gly	Ile	Ser	Leu	Val	Lys	Arg	Glu	Val	Ala	Ser	Val	Cys	Ala	Asp	Ile	Asn	Glu	Trp	Gln	736
2330	CCA	CAG	TTG	GTG	AAT	TGG	CAA	ATG	CAA	TCT	GGT	AAA	GTT	GAC	AAA	CCA	CTG	AGA	CCT	AAA	GCT	CAC	CAC	2398
737	Pro	Gln	Leu	Val	Asn	Trp	Gln	Met	Gln	Ala	Ser	Gly	Lys	Val	Asp	Lys	Pro	Leu	Arg	Pro	Lys	Ala	His	759
2399	CTC	TGG	TGT	GCT	TCT	GGT	CAG	AAG	ATT	ACT	TCA	ATC	AAA	TTT	GCA	AGC	TTT	GGA	ACA	CCA	GGG	GTC	2467	
760	Leu	Leu	Ser	Cys	Ala	Ser	Gly	Gln	Ile	Thr	Ser	Ile	Lys	Phe	Ala	Ser	Phe	Gly	Thr	Pro	Gln	Gly	Val	782
2468	TGC	GGA	AGC	TTC	CGT	GAA	GGA	AGC	TGC	CAC	GCC	TTC	CAC	TCA	TAT	GAT	GCT	TTT	GAA	AGG	TAT	TGC	ATC	2536
783	Cys	Gly	Ser	Phe	Arg	Glu	Gly	Ser	Cys	His	Ala	Phe	His	Ser	Tyr	Asp	Ala	Phe	Glu	Arg	Tyr	Cys	Ile	805

FIG. 2C-4

FIG. 2C-5

2537	GGG	CAA	AAC	TCG	TGC	TCA	GTA	CCT	GTA	ACA	CCA	GAG	ATC	TTT	GGA	GGT	GAT	CCA	TGT	CCA	CAT	GTT	ATG		
806	Gly	Gln	Asn	Ser	Cys	Ser	Cys	Ser	Val	Pro	Val	Thr	Pro	Glu	Ile	Phe	Gly	Gly	Asp	Pro	Cys	Pro	His	Val	Met
2606	AAG	AAA	CTA	CTC	TCA	GTT	GAG	GTT	ATT	TGC	AGT	TGA	TGACACTGAGGAGAACAAATAAAAGTGGTTCAAGTTAGTTGCTGAA	2686											
829	Lys	Lys	Leu	Ser	Val	Glu	Val	Ile	Cys	Ser	***	840													
2687	CATAT	CAAAAGT	GGCTTGATGGAGGTGAAGTTGTACAGATATGCAACACACCTTCCATTGAGGCACATATGAATTGCAATGGCCCAA	2778																					
2779	GATTCTGTACAT	ATATGTTGGTTACTGTCAGTTGGTATTGGTAAATGTAAGTGGTATTGTTGCAAGTAAACAGTAGTATAGTCATTGGTCAAGTGGCATCGAG	2870																						
2871	ATTTGTCAGTGGGAGGTAGTAGGTACCGATCGATCTATGTTGCAACAAAGCTGGGCCTAGATTCCACTATTATTAAACAAGAAAGC	2962																							
2963	ACAATGAGACTGATTAGTCCATGTTGATATTGTTACTGTTGGAATTGGCAAAATCTTGTGATTTCAGCAAAAAAA	3054																							
3055	AAAAAAAAAAAAAA	3069																							

FIG. 2D-1

1	AAAAAAAGTTCAATTTCCTAAAAATAAAAAAATCATTTCATTGAAAAA	63
64	ATG CTA AGG ACT AAT GTG TTG TTA GTT ATT TGT TTA TTG GAT TTT TCT TCA GTG AAA GCT	132
1	Met Leu Arg Thr Asn Val Ile Cys Leu Leu Val Ile Cys Leu Leu Asp Phe Ser Ser Val Lys Ala	23
133	AGT GTT TCT TAT GAT GAC AGA GCT ATA ATC ATA AAT GGG AAA AGA AAA ATT CTT ATT TCT GGT TCA ATT	201
24	Ser Val Ser Tyr Asp Asp Arg Ala Ile Ile Asn Gly Lys Arg Lys Ile Leu Ile Ser Gly Ser Ile	46
202	CAT TAT CCA AGA AGC ACT CCA CAG ATG TGG CCT GAT CTT ATA CAA AAG GCT AAA GAT GGA GGC TTA GAT	270
47	His Tyr Pro Arg Ser Thr Pro Gln Met Trp Pro Asp Leu Ile Gln Lys Ala Lys Asp Gly Gly Leu Asp	69
271	GTT ATT GAA ACT TAT GTT TTC TGG AAT GGA CAT GAG CCT CCT CCT GGA AAA TAT AAT TTT GAA GGA AGA	339
70	Val Ile Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Lys Tyr Asn Phe Glu Gly Arg	92
340	TAT GAT CTT GTT AGA TTC ATC AAA ATG GTA CAA AGA GCA GGA CTT TAT GTC AAT TTA CGT ATT GGC CCT	408
93	Tyr Asp Leu Val Arg Phe Ile Lys Met Val Gln Arg Ala Gly Leu Tyr Val Asn Leu Arg Ile Gly Pro	115

409	TAC	GTC	TGT	GCT	GAA	TGG	AAC	TTT	GGG	GGA	TTC	CCT	GTT	TGG	CTA	AAA	TAT	GTG	CCT	GGT	ATG	GAA	TTT	477
116	Tyr	Val	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Phe	Pro	Val	Trp	Leu	Lys	Tyr	Val	Pro	Gly	Met	Glu	Phe	138
478	AGA	ACA	AAC	AAT	CAG	CCT	TTT	AAG	GTG	GCT	ATG	CAA	GGG	TTT	GTT	CAG	AAA	ATA	GTC	AAC	ATG	ATG	AAG	546
139	Arg	Thr	Asn	Asn	Gln	Pro	Phe	Lys	Val	Ala	Met	Gln	Gly	Phe	Val	Gln	Lys	Ile	Val	Asn	Met	Met	Lys	161
547	TCA	GAA	AAT	TTG	TTT	GAA	TCT	CAA	GGA	CCA	ATA	ATT	ATG	GCC	CAG	ATA	GAA	AAT	GAG	TAT	GGA	CCA	615	
162	Ser	Glu	Asn	Ile	Phe	Glu	Ser	Gln	Gly	Gly	Pro	Ile	Ile	Met	Ala	Gln	Ile	Glu	Asn	Glu	Tyr	Gly	Pro	184
616	GTA	GAA	TGG	GAA	ATT	GGT	GCT	GGT	AAA	GCT	TAT	ACA	AAA	TGG	GCA	GCT	CAA	ATG	GCT	GTA	GGT	TTG	684	
185	Val	Glu	Trp	Glu	Ile	Gly	Ala	Pro	Gly	Lys	Ala	Tyr	Thr	Lys	Trp	Ala	Ala	Gln	Met	Ala	Val	Gly	Leu	207
685	AAA	ACT	GGT	GTC	CCA	TGG	ATC	ATG	TGT	AAG	CAA	GAG	GAT	GCT	CCT	GAT	CCT	GTG	ATT	GAT	ACT	TGT	AAT	753
208	Lys	Thr	Gly	Val	Pro	Trp	Ile	Met	Cys	Lys	Gln	Glu	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asp	Thr	Cys	Asn	230
754	GGC	TTC	TAC	TGC	GAA	GGG	TTC	CGT	CCT	AAT	AAG	CCT	TAC	AAA	CCT	AAA	ATG	TGG	ACA	GAA	GTA	TGG	ACT	822
231	Gly	Phe	Tyr	Cys	Glu	Gly	Phe	Arg	Pro	Asn	Lys	Pro	Tyr	Lys	Pro	Lys	Met	Trp	Thr	Glu	Val	Trp	Thr	253
823	GGC	TGG	TAT	ACG	AAA	TTC	GGT	CCA	ATT	CCC	CAA	AGA	CCA	GCC	GAA	GAC	ATT	GCA	TTT	TCA	GTT	GCC	891	
254	Gly	Trp	Tyr	Thr	Lys	Phe	Gly	Gly	Pro	Ile	Pro	Gln	Arg	Pro	Ala	Gly	Asp	Ile	Ala	Phe	Ser	Val	Ala	276
892	AGG	TTT	GTT	CAG	AAC	AAT	GGT	TCA	TTC	TTC	AAT	TAC	TAC	ATG	TAT	CAT	GGA	GGA	ACA	AAT	TTT	GGC	CGG	960
277	Arg	Phe	Val	Gln	Asn	Asn	Gly	Ser	Phe	Phe	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	299
961	ACA	TCA	TCA	GGG	CTT	TTC	ATT	GCA	ACT	AGC	TAC	GAT	TAT	GCT	CTC	GAT	GAA	TAT	GGG	TTG	CTG	1029		
300	Thr	Ser	Ser	Gly	Leu	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr	Gly	Leu	Leu	322

FIG. 2D-2

1030	AAT	CCA	AAG	TAT	GGG	CAC	TTG	AGA	GAC	TTA	CAT	AAA	GCT	ATC	AAG	CTA	TCT	GAA	CCG	GCT	TTA	GTT	1098	
323	Asn	Glu	Pro	Lys	Tyr	Gly	His	Leu	Arg	Asp	Leu	His	Lys	Ala	Ile	Lys	Leu	Ser	Glu	Pro	Ala	Leu	Val	345
1099	TCA	TCA	TAT	GCT	GCG	GTG	ACT	AGT	CTT	GGA	AGT	AAT	CAA	GAG	GCT	CAT	GTT	TAT	AGA	TCA	AAA	TCT	GGA	1167
346	Ser	Ser	Tyr	Ala	Ala	Val	Thr	Ser	Leu	Gly	Ser	Asn	Gln	Glu	Ala	His	Val	Tyr	Arg	Ser	Lys	Ser	Gly	368
1168	GCT	TGT	GCT	GCT	TTT	TTA	TCC	AAC	TAT	GAC	TCT	AGA	TAT	TCA	GTA	AAA	GTC	ACC	TTT	CAG	AAT	AGG	CCA	1236
369	Ala	Cys	Ala	Ala	Phe	Leu	Ser	Asn	Tyr	Asp	Ser	Arg	Tyr	Ser	Val	Iys	Val	Thr	Phe	Gln	Asn	Arg	Pro	391
1237	TAC	AAT	CTG	CCT	CCA	TGG	TCC	ATC	AGC	ATT	CTT	CCC	GAC	TGC	AAA	ACT	GCC	GTT	TAC	AAC	ACT	GCA	CAG	1305
392	Tyr	Asn	Ieu	Pro	Pro	Trp	Ser	Ile	Ser	Ile	Leu	Pro	Asp	Cys	Iys	Thr	Ala	Val	Tyr	Asn	Thr	Ala	Gln	414
1306	GTT	AAC	TCT	CAA	AGC	TCG	AGC	ATA	AAG	ATG	ACG	CCT	GCA	GGT	GGT	GGG	TTG	TCT	TGG	CAG	TCA	TAC	AAT	1374
415	Val	Asn	Ser	Gln	Ser	Ser	Ser	Ile	Lys	Met	Thr	Pro	Ala	Gly	Gly	Gly	Ieu	Ser	Trp	Gln	Ser	Tyr	Asn	437
1375	GAA	GAA	ACG	CCT	ACT	GCT	GAT	GAC	AGC	GAT	ACA	CTT	ACA	GCT	AAC	GGA	CTA	TGG	GAA	CAG	AAA	AAC	GTC	1443
438	Glu	Glu	Thr	Pro	Thr	Ala	Asp	Asp	Asp	Ser	Asp	Thr	Leu	Thr	Ala	Asn	Gly	Leu	Trp	Glu	Gln	Lys	Asn	460
1444	ACA	AGA	GAT	TCA	TCA	GAC	TAT	CTG	TGG	TAC	ATG	ACA	AAT	GTA	AAT	ATA	GCA	TCT	ATAT	GAA	GGA	TTT	CTA	1512
461	Thr	Arg	Asp	Ser	Ser	Asp	Tyr	Leu	Trp	Tyr	Met	Thr	Asn	Val	Ile	Ala	Ser	Asn	Glu	Gly	Phe	Leu	483	
1513	AAG	AAC	GGA	AAG	GAT	CCT	TAT	CTC	ACT	GTT	ATG	TCC	GCT	GGT	CAT	GTC	TTG	CAT	GTT	TTC	GTC	AAT	GGA	1581
484	Lys	Asn	Gly	Lys	Asp	Pro	Tyr	Leu	Thr	Val	Met	Ser	Ala	Gly	His	Val	Leu	His	Val	Phe	Val	Asn	Gly	506
1582	AAA	CTA	TCA	GGA	ACT	GTT	TAT	GGT	ACA	TTC	GAT	AAT	CCA	AAA	CTT	ACA	TAC	AGT	GGC	AAC	GTG	AAG	TTA	1650
507	Lys	Leu	Ser	Gly	Thr	Val	Tyr	Gly	Thr	Leu	Asp	Asn	Pro	Lys	Leu	Thr	Tyr	Ser	Gly	Asn	Val	Lys	Leu	529

FIG. 2D-3

1651	AGA	GCT	GGT	ATT	AAC	AAG	ATT	TCT	CTG	CTC	AGT	GTT	TCC	GGT	CTC	CCG	AAC	GTT	GGC	GTG	CAT	TAT	1719	
530	Arg	Ala	Gly	Ile	Asn	Lys	Ile	Ser	Leu	Leu	Ser	Val	Ser	Vai	Gly	Leu	Pro	Asn	Val	Gly	Val	His	Tyr	552
1720	GAT	ACA	TGG	AAT	GCA	GGG	GTT	CTA	GGT	CCA	GTC	ACG	TTG	AGC	GGT	CTC	AAT	GAA	GGG	TCA	AGA	AAC	TTG	1788
553	Asp	Thr	Trp	Asn	Ala	Gly	Val	Leu	Gly	Pro	Val	Thr	Leu	Ser	Gly	Leu	Asn	Glu	Gly	Ser	Arg	Asn	Leu	575
1789	GCG	AAA	CAG	AAA	TGG	TCT	TAC	AAG	GTT	GGT	CTG	AAA	GGC	GAA	TCG	TTA	AGT	CTT	CAC	TCC	TTA	AGT	GGG	1857
576	Ala	Lys	Gln	Lys	Trp	Ser	Tyr	Lys	Val	Gly	Leu	Lys	Gly	Glu	Ser	Leu	Ser	Leu	His	Ser	Leu	Ser	Gly	598
1858	AGT	TCT	TCT	GTT	GAA	TGG	GTT	CGA	GGT	TCA	CTA	ATG	GCT	CAA	AAG	CAG	CCC	CTG	ACT	TGG	TAC	AAG	GCT	1926
599	Ser	Ser	Ser	Val	Glu	Trp	Val	Arg	Gly	Ser	Leu	Met	Ala	Gln	Lys	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	Ala	621
1927	ACA	TTT	AAC	GCG	CCT	GGG	GGG	AAT	GAT	CCA	CTA	GCT	TTA	GAC	ATG	GCA	AGT	ATG	GGA	AAA	GGT	CAG	ATA	1995
622	Thr	Phe	Asn	Ala	Pro	Gly	Gly	Asn	Asp	Pro	Leu	Ala	Ieu	Asp	Met	Ala	Ser	Met	Gly	Lys	Gly	Gln	Ile	644
1996	TGG	ATA	AAT	GGT	GAA	GGC	GTA	GGT	CGC	CAT	TGG	CCT	GGA	TAC	ATA	GCA	CAA	GGC	GAC	TGC	AGC	AAA	TGC	2064
645	Trp	Ile	Asn	Gly	Glu	Gly	Val	Gly	Arg	His	Trp	Pro	Gly	Tyr	Ile	Ala	Gln	Gly	Asp	Cys	Ser	Lys	Cys	667
2065	AGT	TAT	GCT	GGA	ACG	TTC	AAC	GAG	AAG	TGC	CAG	ACT	AAC	TGC	GGA	CAA	CCT	TCT	CAG	AGA	TGG	TAC	2133	
668	Ser	Tyr	Ala	Gly	Thr	Phe	Asn	Glu	Lys	Lys	Cys	Gln	Thr	Asn	Cys	Gly	Gln	Pro	Ser	Gln	Arg	Trp	Tyr	690
2134	CAT	GTT	CCA	CGG	TCG	TGG	CTG	AAA	CCA	AGT	GGG	AAC	TTG	TTA	GTA	TTC	GAA	GAA	TGG	GGA	GGT	AAT	2202	
691	His	Val	Pro	Arg	Ser	Trp	Leu	Lys	Pro	Ser	Gly	Asn	Leu	Leu	Val	Val	Phe	Glu	Glu	Trp	Gly	Gly	Asn	713
2203	CCA	ACA	GGA	ATT	TCT	CTA	GTC	AGG	AGA	TCA	AGA	TAA	AGAACTCGAAAAGTAAACTTGTTCAGTA	TTGCTTGA	A									2282
714	Pro	Thr	Gly	Ile	Ser	Leu	Val	Arg	Arg	Ser	Arg	***											725	

FIG. 2D-4

2283	TTCGGCCGAAATACACGAAGCTAACATGGAGGCTACAGTTGCCAATTGCAGCTGAATAAACATAGAACATAAGAAATT	2374
2375	TGATTAAAGGAGTATATAAATTACAGAGAATTTCCTTATTCTTGTTAAACTTGTATAAGTTTACAGAATTTCGTATT	2466
2467	GGATTATGAGATTGAAAGATTGACAGCTTCCAAATACATTAGAACATAAAATTCAATTGTA	2554

FIG. 2D-5

1	ATC	CAG	ACT	TAC	GTT	TTC	TGG	AAC	CTT	CAT	GAA	CCT	GTT	CGA	AAT	CAG	TAT	GAT	TTT	GAA	GGA	AGG	AAA	69	
1	Ile	Gln	Thr	Tyr	Val	Tyr	Val	Asn	Leu	His	Glu	Pro	Val	Arg	Asn	Gln	Tyr	Asp	Phe	Glu	Gly	Arg	Lys	23	
70	GAT	TTG	ATT	AAT	TTT	GTG	AAG	TTG	GAG	AGA	GCT	GGC	TTA	TTT	GTT	CAT	ATA	AGG	ATT	GGG	CCT	TAT		138	
24	Asp	Leu	Ile	Asn	Phe	Val	Lys	Leu	Val	Glu	Arg	Ala	Gly	Leu	Phe	Val	His	Ile	Arg	Ile	Gly	Pro	Tyr	46	
1139	GTT	TGT	GCA	GAA	TGG	AAC	TAT	GGT	GGG	TTT	CCT	CTT	TGG	TTG	CAT	TTC	ATT	CCT	CGA	ATT	GAA	TTT	CGA		207
47	Val	Cys	Ala	Glu	Glu	Trp	Asn	Tyr	Gly	Gly	Phe	Pro	Leu	Trp	Leu	His	Phe	Ile	Pro	Gly	Ile	Glu	Phe	Arg	69
208	ACC	GAC	AAT	GAA	CCG	TTC	AAG	GCA	GAA	ATG	AAG	CGA	TTC	ACA	GCT	AAA	ATT	GTT	GAC	ATG	ATC	AAG	CAA		276
70	Thr	Asp	Asn	Glu	Pro	Phe	Lys	Ala	Glu	Met	Lys	Arg	Phe	Thr	Ala	Lys	Ile	Val	Asp	Met	Ile	Lys	Gln	92	
277	GAA	AAT	CTA	TAT	GCA	TCC	CAG	GGT	GGG	CCG	GTT	ATC	TTG	TCT	CAG	ATA	GAA	AAT	GAG	TAT	GGC	AAT	GGT		345
93	Glu	Asn	Leu	Tyr	Ala	Ser	Gln	Gly	Gly	Pro	Val	Ile	Leu	Ser	Gln	Ile	Glu	Asn	Glu	Tyr	Gly	Asn	Gly	115	
346	GAT	ATT	GAG	TCT	CGT	TAT	GGT	CCT	CGT	GCC	AAA	CCU	TAC	GTG	AAC	TGG	GCA	GCA	TCA	ATG	GCT	ACG	TCT		414
1116	Asp	Ile	Glu	Ser	Arg	Tyr	Gly	Pro	Arg	Ala	Lys	Pro	Tyr	Val	Asn	Trp	Ala	Ala	Ser	Met	Ala	Thr	Ser	138	
4115	TTA	AAT	ACG	GGA	GTC	CCA	TGG	GTT	ATG	TGT	CAG	CAA	GAT	GCC	CCT	CCT	TCC	GTT	ATT	AAC	ACT	TGC		483	
1139	Leu	Asn	Thr	Gly	Val	Pro	Trp	Val	Met	Cys	Gln	Gln	Pro	Asp	Ala	Pro	Pro	Ser	Val	Ile	Asn	Thr	Cys	161	
484	AAT	GGA	TTT	TAT	TGT	GAC	CAA	TTC	AAG	CAA	AAT	TCC	GAT	AAA	ACA	CCC	AAG	ATG	TGG	ACT	GAG	AAT	TGG		552
1162	Asn	Gly	Phe	Tyr	Cys	Asp	Gln	Phe	Lys	Gln	Asn	Ser	Asp	Lys	Thr	Pro	Lys	Met	Trp	Thr	Glu	Asn	Trp	184	

FIG. 2E

FIG. 2E-2

553	ACC	GGA	TGG	TTT	CTG	TCG	TTT	GGT	GGT	CCT	GTC	CCT	TAC	AGA	CCA	GTG	GAA	GAC	ATC	GCT	TTC	GCT	GTG		
185	Thr	Gly	Trp	Phe	Leu	Ser	Phe	Gly	Gly	Pro	Val	Pro	Tyr	Arg	Pro	Val	Glu	Asp	Ile	Ala	Phe	Ala	Val	207	
622	GCT	CGA	TTT	TTC	CAG	CGA	GGC	GGG	GGG	ACT	TTC	CAG	AAC	TAT	TAC	ATG	TAC	CAC	GGG	GGA	ACT	AAC	TTT	GGG	
208	Ala	Arg	Phe	Phe	Gln	Arg	Gly	Gly	Gly	Thr	Phe	Gln	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	230
691	AGA	ACC	AGT	GGT	GGA	CCG	TTT	ATT	GCA	ACT	AGC	TAT	GAC	TAT	GAT	GCC	CCT	CTC	GAC	GAA	TAC	GG	755		
231	Arg	Thr	Ser	Gly	Gly	Pro	Phe	Ile	Ala	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr	252			

1	ATC	CAG	ACA	TAT	GTT	TTT	TGG	AAT	GTT	CAT	GAG	CCT	TCT	CCT	GGC	AAT	TAC	AAT	TTT	GAA	GGA	AGA	TAT	69	
1	Ile	Gln	Thr	Tyr	Val	Phe	Trp	Asn	Val	His	Glu	Pro	Ser	Pro	Gly	Asn	Tyr	Asn	Pro	Glu	Gly	Arg	Tyr	23	
70	GAC	CTG	GTG	AGG	TTT	GTA	AAA	ACG	ATT	CAG	AAA	GCA	GGG	CTG	TAT	GCT	CAT	CTT	CGA	ATT	GGC	CCT	TAC	138	
24	Asp	Leu	Val	Arg	Phe	Val	Lys	Thr	Ile	Gln	Lys	Ala	Gly	Leu	Tyr	Ala	His	Leu	Arg	Ile	Gly	Pro	Tyr	46	
139	GTT	TGT	GCA	GAG	TGG	TGG	AAT	TTT	GGA	GGG	TTT	CCA	GTA	TGG	CTG	AAG	TAT	GTA	CCT	GGC	ATT	AGC	TTC	AGA	207
47	Val	Cys	Ala	Glu	Trp	Asn	Phe	Gly	Gly	Gly	Pro	Val	Trp	Leu	Lys	Tyr	Val	Pro	Gly	Ile	Ser	Phe	Arg	69	
208	GCT	GAT	AAT	GAA	CCT	TTC	AAG	AAC	GCA	ATG	AAA	GGG	TAT	GCT	GAG	AAA	ATT	GTT	AAC	TTG	ATG	AAG	ATC	276	
70	Ala	Asp	Asn	Glu	Pro	Phe	Lys	Asn	Ala	Met	Lys	Gly	Tyr	Ala	Glu	Lys	Ile	Val	Asn	Leu	Met	Lys	Ile	92	
277	ATA	ATC	TTT	TCG	AGT	CTC	AGG	GTG	GTC	CAA	TCA	TAC	TCT	CAC	AGA	TTG	AGA	ATG	AGT	ATG	GGC	CTC	AAG	345	
93	Ile	Ile	Phe	Ser	Ser	Leu	Arg	Val	Val	Gln	Ser	Tyr	Ser	His	Arg	Leu	Arg	Met	Ser	Met	Gly	Leu	Lys	115	
346	CCA	AGG	TAC	TTG	GAG	CAC	CGG	GAC	ATC	AGT	ATT	CAA	CAT	GGG	CTG	CAA	ATA	TGG	CAG	TTG	GAT	TTG	AAC	414	
116	Pro	Arg	Tyr	Leu	Glu	His	Arg	Asp	Ile	Ser	Ile	Gln	Ile	Gly	Leu	Gln	Ile	Trp	Gln	Ile	Asp	Leu	Asn	138	

FIG. 2F-1

FIG. 2F-2

415	ACA	GGC	GTC	CCA	TGG	GTG	ATG	TGC	AAG	GAA	GAT	GCA	CCA	GAT	CCT	GTG	ATC	AAC	ACA	TGC	AAT	GGT	
139	Thr	Gly	Val	Pro	Trp	Val	Met	Cys	Lys	Glu	Glu	Asp	Ala	Pro	Asp	Pro	Val	Ile	Asn	Thr	Cys	Asn	Gly
484	TTC	TAC	TGT	GAT	AAT	TTC	TTC	CCA	AAC	AAA	CCA	TAC	AAA	CCT	GCA	ATT	TGG	ACT	GAA	GCT	TGG	AGT	GGA
162	Phe	Tyr	Cys	Asp	Asn	Phe	Phe	Pro	Asn	Lys	Pro	Tyr	Lys	Pro	Ala	Ile	Trp	Thr	Glu	Ala	Trp	Ser	Gly
553	TGG	TTC	TCG	GAA	TTT	GGC	GGT	CCC	CTT	CAT	CAG	AGA	CCA	GTT	CAG	GAT	TTG	GCA	TTC	GCT	GTC	CAA	
185	Trp	Phe	Ser	Glu	Phe	Gly	Gly	Pro	Ile	His	Gln	Arg	Pro	Val	Gln	Asp	Leu	Ala	Phe	Ala	Val	Ala	Gln
622	TTT	ATA	CAA	AGA	GGA	GGA	TCT	TCT	GTT	AAC	TAT	TAC	ATG	TAC	CAT	GGG	GGC	ACG	AC	TTT	GGA	CGC	ACT
208	Phe	Ile	Gln	Arg	Gly	Gly	Ser	Phe	Val	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr
691	GCG	GGT	GGG	CCA	TTC	ATC	ACT	ACC	AGC	TAT	GAT	TAT	GAT	GCC	CCC	CTC	GAC	GAG	TAT	GG			
231	Ala	Gly	Gly	Pro	Phe	Ile	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Leu	Asp	Glu	Tyr					

FIG. 2G-1

311	CCT CGC AGT GTC CCT GCC ATG TGG CCT GGT CTG GTT CGA TTG GCG AAG GAA GGA GGA GTG GAT GTT ATT		379
70	Pro Arg Ser Val Pro Ala Met Trp Pro Gly Leu Val Arg Leu Ala Lys Glu Gly Val Asp Val Ile		92
380	GAA ACC TAT GTT TTC TGG AAC GGT CAC GAA CCT TCT CCG GGC AAT TAT TAC TTT GGA GGA AGG TTT GAT		448
93	Glu Thr Tyr Val Phe Trp Asn Gly His Glu Pro Ser Pro Gly Asn Tyr Tyr Phe Gly Gly Arg Phe Asp		115
449	CTA GTC AAA TTT TGT AAG ATC ATT CAG CAG GCT GGA ATG TAT ATG ATT CTT CGG ATT GGA CCA TTT GTA		517
116	Leu Val Lys Phe Cys Lys Ile Ile Gln Gln Ala Gly Met Tyr Met Ile Leu Arg Ile Gly Pro Phe Val		138
518	GCT GCA GAA TGG AAC TTT GGT GGA CTT CCT GTG TGG TTG CAT TAT GTG CCA GGT ACC ACC TTT CGG ACT		586
139	Ala Ala Glu Trp Asn Phe Gly Gly Leu Pro Val Trp Leu His Tyr Val Pro Gly Thr Phe Arg Thr		161
587	GAT AGT GAA CCA TTT AAG TAT CAC ATG CAG AAG TTC ATG ACA TAT ACA GTG AAC TTA ATG AAG AGA GAG		655
162	Asp Ser Glu Pro Phe Lys Tyr His Met Gln Lys Phe Met Thr Tyr Thr Val Asn Leu Met Lys Arg Glu		184
656	AGG CTT GCA TCT CAA GGA GGT CCA ATC ATC TTG TCA CAG GTA GAA AAT GAG TAC GGC TAC TAT GAA		724
185	Arg Leu Phe Ala Ser Gln Gly Gly Pro Ile Ile Leu Ser Gln Val Glu Asn Glu Tyr Gly Tyr Try Glu		207
725	AAT GCA TAT GGA GAA GGA GGG AAA AGG TAT GCC TTA TGG GCT GCT AAA ATG GCC CTT TCT CAA AAT ACT		793
208	Asn Ala Tyr Gly Glu Gly Gly Lys Arg Tyr Ala Leu Trp Ala Ala Lys Met Ala Leu Ser Gln Asn Thr		230
794	GGT GTA CCT TGG ATA ATG TGC CAG TAT GAT GCT CCT GAT CCT GTG ATT GAC ACA TGC AAT TCA TTT		862
231	Gly Val Pro Trp Ile Met Cys Gln Gln Tyr Asp Ala Pro Asp Pro Val Ile Asp Thr Cys Asn Ser Phe		253
863	TAC TGC GAC CAA TTT AAA CCA ATC TCT CCA AAC AAG CCC AAA ATT TGG ACA GAG AAC TGG CCG GGA TGG		931
254	Tyr Cys Asp Gln Phe Lys Pro Ile Ser Pro Asn Lys Pro Lys Ile Trp Thr Glu Asn Trp Pro Gly Trp		276

FIG. 2G-2

932	TTC	AAG	ACA	TTT	GGG	GCC	AGA	GAT	CCT	CAC	AGG	CCT	GCA	GAA	GAT	GTT	GCT	TAT	TCC	GTG	GCT	CGT	TTT	1000	
277	Phe	Lys	Thr	Phe	Gly	Ala	Arg	Asp	Pro	His	Arg	Pro	Ala	Glu	Asp	Val	Ala	Tyr	Ser	Val	Ala	Arg	Phe	299	
1001	TTC	CAA	AAA	GGA	GGG	AGC	GTC	CAG	AAT	TAT	TAC	ATG	TAC	CAT	GGT	GGG	ACG	AAC	TTT	GGC	AGG	ACA	GCA	1069	
300	Phe	Gln	Lys	Gly	Gly	Ser	Val	Gln	Asn	Tyr	Tyr	Met	Tyr	His	Gly	Gly	Thr	Asn	Phe	Gly	Arg	Thr	Ala	322	
1070	GGT	GGC	CCT	TTC	ATT	ACC	ACA	AGT	TAT	GAC	TAT	GAT	GCC	CCA	ATT	GAC	GAA	TAT	GTG	TTA	CCA	AGG	TTT	1138	
323	Gly	Gly	Pro	Phe	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Asp	Glu	Tyr	Gly	Leu	Pro	Arg	Phe	345	
1139	CCA	AAA	TGG	GGT	CAC	CTT	AAA	GAA	CTT	CAT	AAA	GTC	ATA	AAA	TCG	TGT	GAG	CAT	GCT	CTG	CTG	AAC	AAT	1207	
346	Pro	Lys	Trp	Gly	His	Leu	Lys	Glu	Leu	His	Lys	Val	Ile	Lys	Ser	Cys	Glu	His	Ala	Leu	Leu	Asn	Asn	368	
1208	GAT	CCA	ACT	CTT	CTT	TCA	TTA	GGT	CCT	CTA	CAA	GAG	GCT	GAT	GTT	TAT	GAA	GAT	GCT	CTG	CTG	AAC	AAT	1276	
369	Asp	Pro	Thr	Ile	Leu	Leu	Ser	Leu	Gly	Pro	Leu	Gln	Glu	Ala	Asp	Val	Tyr	Glu	Asp	Ala	Ser	Gly	Ala	Cys	391
1277	GCT	GCC	TTT	CTC	GCG	AAT	ATG	GAT	GAC	AAA	AAT	GAC	AAG	GTG	GTA	CAG	TTC	CGA	CAT	GTA	TCA	TAC	CAC	1345	
392	Ala	Ala	Phe	Ile	Ala	Asn	Met	Asp	Asp	Asp	Lys	Asn	Asp	Lys	Val	Val	Gln	Phe	Arg	His	Val	Ser	Tyr	His	414
1346	TTC	CCA	GCA	TGG	TCT	GTT	AGC	ATT	TTG	CCA	GAC	TGC	AAA	AAT	GTA	GCG	TTC	AAC	ACA	GCA	AAG	GTT	GGA	1414	
415	Leu	Pro	Ala	Trp	Ser	Val	Ser	Ile	Ile	Pro	Asp	Cys	Lys	Asn	Val	Ala	Phe	Asn	Thr	Ala	Lys	Val	Gly	437	
1415	TGT	CAA	ACT	TCT	ATT	GTC	AAT	ATG	GCA	CCC	ATA	GAT	TTG	CAT	CCC	ACC	GCA	AGT	TCA	CCA	AAG	AGA	GAC	1483	
438	Cys	Gln	Thr	Ser	Ile	Val	Asn	Met	Ala	Pro	Ile	Asp	Leu	His	Pro	Thr	Ala	Ser	Ser	Pro	Lys	Arg	Asp	460	
1484	ATC	AAG	TCT	CTT	CAG	TGG	GAA	GTC	TTC	AAG	GAA	ACA	GCT	GGA	TGG	GGA	GTT	GCT	GAT	TTC	ACT	AAA	1552		
461	Ile	Lys	Ser	Leu	Gln	Trp	Glu	Val	Phe	Lys	Glu	Thr	Ala	Gly	Val	Trp	Gly	Val	Ala	Asp	Phe	Thr	Lys	483	

FIG. 2G-3

1553	AAC	GGA	TTT	GTA	GAT	CAC	ATT	AAC	ACC	ACA	AAA	GAT	GCT	ACA	GAC	TAC	CTC	TGG	TAC	ACA	AGT	ATT	1621	
484	Asn	Gly	Phe	Val	Asp	His	Ile	Asn	Thr	Thr	Lys	Asp	Ala	Thr	Arg	Tyr	Leu	Trp	Tyr	Thr	Thr	Ser	Ile	506
1622	TTT	GTT	CAT	GCA	GAG	GAT	TTC	CTA	AGA	AAC	AGA	GGC	ACT	GCA	ATG	CTT	TTC	GTT	GAA	TCA	AAG	GGT	1690	
507	Phe	Val	His	Ala	Glu	Glu	Asp	Phe	Leu	Arg	Asn	Arg	Gly	Thr	Ala	Met	Leu	Phe	Val	Glu	Ser	Lys	Gly	529
1691	CAT	GCT	ATG	CAT	GTC	TTC	ATC	AAT	AAA	AAG	CTT	CAA	GCC	AGT	GCA	TCT	GGA	AAT	GGC	ACA	GTG	CCA	CAG	1759
530	His	Ala	Met	His	Val	Phe	Ile	Asn	Lys	Lys	Leu	Gln	Ala	Ser	Ala	Ser	Gly	Asn	Gly	Thr	Val	Pro	Gln	552
1760	TTC	AAG	TTT	GGA	ACT	CCT	ATT	GCT	CTA	AAG	GCA	GGG	AAG	ATT	TCC	TTC	TTA	AGC	ATG	ACT	GTG	1828		
553	Phe	Lys	Phe	Gly	Thr	Pro	Ile	Ala	Leu	Lys	Ala	Gly	Lys	Asn	Glu	Ile	Ser	Leu	Ieu	Ser	Met	Thr	Val	575
1829	GGC	CTA	CAA	ACA	GCT	GGA	GCG	TTT	TAT	GAA	TGG	ATT	GGA	GCT	GGT	CCA	ACA	AGT	GTC	AAA	GTT	GCA	GGG	1897
576	Gly	Leu	Gln	Thr	Ala	Gly	Ala	Phe	Tyr	Glu	Trp	Ile	Gly	Ala	Gly	Pro	Thr	Ser	Val	Lys	Val	Ala	Gly	598
1898	TTC	AAG	ACT	GGG	ACT	ATG	GAC	TTG	ACT	GCG	TCT	GCT	TGG	ACC	TAT	AAG	ATT	GGA	TTG	CAA	GGA	GAA	CAT	1966
599	Phe	Lys	Thr	Gly	Thr	Met	Asp	Leu	Thr	Ala	Ser	Ala	Trp	Thr	Tyr	Lys	Ile	Gly	Leu	Gln	Gly	Glu	His	621
1967	TTG	AGG	ATA	CAG	AAG	TCA	TAT	AAC	TTG	AAG	AGT	AAA	ATT	TGG	GCA	CCA	ACT	TCG	CAG	CCA	CCA	AAG	CAA	2035
622	Leu	Arg	Ile	Gln	Lys	Ser	Tyr	Asn	Leu	Lys	Ser	Lys	Ile	Trp	Ala	Pro	Thr	Ser	Gln	Pro	Pro	Lys	Gln	644
2036	CAG	CCC	CTC	ACA	TGG	TAT	AAG	GCA	GTA	GAT	GGC	CCT	GGT	AAT	GAA	CCT	GTT	GCA	CTT	GAT	ATG	2104		
645	Gln	Pro	Leu	Thr	Trp	Tyr	Lys	Ala	Val	Val	Asp	Ala	Pro	Pro	Gly	Asn	Glu	Pro	Val	Ala	Leu	Asp	Met	667
2105	ATT	CAT	ATG	GGA	AAA	GGA	ATG	GCT	TGG	TTG	AAT	GGA	CAA	GAA	ATT	GGC	AGA	TAT	TGG	CCG	AGG	AGA	ACT	2173
668	Ile	His	Met	Gly	Lys	Gly	Met	Ala	Trp	Leu	Asn	Gly	Gln	Glu	Ile	Gly	Art	Tyr	Trp	Pro	Arg	Arg	Thr	690

FIG. 2G-4

2174	TCT	AAA	TAT	GAG	AAT	TGT	GTT	ACT	CAA	TGT	GAC	TAC	AGA	GCG	AAA	TTT	AAC	CCT	GAT	AAG	TGT	GTC	ACT	2242
691	Ser	Lys	Tyr	Glu	Asn	Cys	Val	Thr	Gln	Cys	Asp	Tyr	Arg	Gly	Lys	Phe	Asn	Pro	Asp	Lys	Cys	Val	Thr	713
2243	GGC	TGT	GGA	CAA	CCT	ACA	CAG	AGA	TGG	TAT	CAT	GTG	CCA	CGA	TCT	TGG	TTC	AAG	CCA	TCA	GGA	AAT	GTC	2311
714	Gly	Cys	Gly	Gln	Pro	Thr	Gln	Arg	Trp	Tyr	His	Val	Pro	Arg	Ser	Trp	Phe	Lys	Pro	Ser	Gly	Asn	Val	736
2312	TTA	ATT	ATC	TTT	GAG	GAA	ATA	GGT	GGA	GAT	CCC	TCT	CAA	ATT	AGA	TTC	TCA	ATG	CGA	AAG	GTT	TCT	GGA	2380
737	Leu	Ile	Ile	Phe	Glu	Glu	Ile	Gly	Gly	Asp	Pro	Ser	Gln	Ile	Arg	Phe	Ser	Met	Arg	Lys	Val	Ser	Gly	759
2381	GCT	TGT	GGT	CAT	CTT	TCA	GTG	GAC	CAT	CCA	TCC	TTT	GAT	GTT	GAA	AAT	CTG	CAA	GGA	AGT	GAA	ATT	GAG	2449
760	Ala	Cys	Gly	His	Leu	Ser	Val	Asp	His	Pro	Ser	Phe	Asp	Val	Glu	Asn	Leu	Gln	Gly	Ser	Glu	Ile	Glu	782
2450	AAC	GAC	AAA	AAC	AGG	CCA	ACT	CTA	AGT	TTG	AAA	TGC	CCC	ACA	AAT	ACT	AAT	ATT	TCC	TCT	GTC	AAA	TTT	2518
783	Asn	Asp	Lys	Asn	Arg	Pro	Thr	Leu	Ser	Leu	Lys	Cys	Pro	Thr	Asn	Thr	Asn	Ile	Ser	Ser	Val	Lys	Phe	805
2519	GCC	AGC	TTT	GGA	AAT	CCT	AAT	GGT	ACA	TGT	GGC	TCC	TAC	ATG	CTA	GGA	GAC	TGC	CAC	GAT	CAG	AAT	TCT	2587
806	Ala	Ser	Phe	Gly	Asn	Pro	Asn	Gly	Thr	Cys	Gly	Ser	Tyr	Met	Leu	Gly	Asp	Cys	His	Asp	Gln	Asn	Ser	828
2588	GCA	GCA	CTG	GTC	GAA	AAG	GTT	TGC	CTG	AAC	CAA	AAT	GAG	TGT	GCA	TAA	ATG	TCC	AGC	GCA	AAC	TTT	2656	
829	Ala	Ala	Leu	Val	Glu	Lys	Val	Cys	Ieu	Asn	Gln	Asn	Glu	Cys	Ala	Leu	Glu	Met	Ser	Ser	Ala	Asn	Phe	851
2657	AAC	ATG	CAA	TTG	TGT	CCA	AGT	ACA	GTA	AAG	AAA	CTT	GCA	GTT	GAA	GTG	AAT	TGC	AGC	TGA	GTGT	CATTGCC	2728	
852	Asn	Met	Gln	Ieu	Cys	Pro	Ser	Thr	Val	Lys	Lys	Leu	Ala	Val	Glu	Val	Asn	Cys	Ser	***			871	
2729	AAA	ATG	AA	CAT	ATT	TCT	A	TT	AT	AGT	TTG	GAG	ATG	CTT	AA	AC	CTT	TCT	AT	AGC	AAA	AA	ACT	2820
2821	CTT	TC	G	T	C	T	A	T	T	G	A	G	T	T	A	A	C	C	T	A	C	C	AA	2912
2913	GT	ATT	C	A	T	T	A	T	T	G	A	G	T	T	G	A	G	T	T	G	A	G	AA	2972

FIG. 2G-5

		10	20	30	40	50
TBG1-ORF	-24	MGFWM	MLLMLLLCLW	VSCGISVSYD
TBG2-ORF	-14	MSRRKT	LNFPLILTVL	TIHFIVAGE	YFKPFNVTYD
TBG3-ORF	-20	MGCTLILMLN	VLLVLLGSWV	FSGTASVSYD
TBG4-ORF	-22MLRTNVLL	LLVICLLDFF	SSVKASVSYD
TBG5-ORF	1	-----	-----	-----	-----	-----
TBG6-ORF	1	-----	-----	-----	-----	-----
TBG7-ORF	-1	.MNTMSCLSS	NFKFVFLAST	VIWMTVMSS	LAADVASNVT	TIGTDSVTYD
apple	-21MGVGIQTMW	SILLLFSCIF	SAASASVSYD
carnation	-16	MLCG	KENNVMKML	VYVFVLITLI
asparagus	-20	VALLAAVWSP	PAVTASVTYD
broccoli	-20	MALKVLMLM	-----
Lupin	-12MFGSRIVM	ESLMSRRNFH	MVLLLLFFWV	CYVTASVTYD
		60	70	80	90	100
TBG1-ORF	27	HKAIIVNGQR	KILISGSIHY	PRSTPEMWPD	LIQKAKEGGV	DVIQTYVFWN
TBG2-ORF	37	NRALIIGGKR	RMLISAGIH	PRATPEMWPT	LIARSKEGGA	DVIETYTFWN
TBG3-ORF	31	HRAIIIVNGQR	RILISGSVHY	PRSTPEMWPG	IIQKAKEGGV	DVIQTYVFWN
TBG4-ORF	29	DRAIIINGKR	KILISGSIHY	PRSTPQMWP	LIQKAKDGGL	DVIETYVFWN
TBG5-ORF	51	-----	-----	-----	-----	--IQTYVFWN
TBG6-ORF	51	-----	-----	-----	-----	--IQTYVFWN
TBG7-ORF	50	RRSLIINGQR	KLLISASIHY	PRSVPAMWPG	LVRLAKEGGV	DVIETYVFWN
apple	30	HKAIINGQK	RILISGSIHY	PRSTPEMWPD	LIQKAKDGGL	DVIQTYVFWN
carnation	35	YRAIKINDQR	RILLSGSIHY	PRSTPEMWPD	IIEKAKDSQL	DVIQTYVFWN
asparagus	31	HKSVIINGQR	RILISGSIHY	PRSTPEMWPD	LIQKAKDGGL	DVIQTYVFWN
broccoli	31	ERAITIDGQR	RILLSGSIHY	PRSTSMDMWP	LISKAKDGGL	DTIETYVFWN
Lupin	39	HKAIMINGQR	RILISGSIHY	PRSTPQMWP	LIQKAKDGGL	DVIETYVFWN
		110	120	130	140	150
TBG1-ORF	77	GHEPEEGKYY	FEERYDLVKF	IKVVQEAGLY	VHLRIGPYAC	AEWNFGGFV
TBG2-ORF	87	GHEPTRGQYM	FEGRYDIVKF	AKLVGSHGLF	LFIRIGPYAC	AEWNFGGFPI
TBG3-ORF	81	GHEPQQGKYY	FEGRYDLVKF	IKLVHQAGLY	VHLRVGPYAC	AEWNFGGFV
TBG4-ORF	79	GHEPSPGKYN	FEGRYDLVRF	IKMVQRAGLY	VNLRIGPYVC	AEWNFGGFV
TBG5-ORF	101	LHEPVRNQYD	FEGRKDLINE	VKLVERAGLF	VHIRIGPYVC	AEWNYGGFP
TBG6-ORF	101	VHEPSPGNYN	FEGRYDLVRF	VKTIQKAGLY	AHLRIGPYVC	AEWNFGGFV
TBG7-ORF	100	GHEPSPGNYY	FGGRFDLVKF	CKIIQQAGMY	MILRIGPFVA	AEWNFGGLPV
apple	80	GHEPSPGNYY	FEERYDLVKF	IKLVQQEGLF	VNLRIGPYVC	AEWNFGGFV
carnation	85	GHEPSEGKYY	FEGRYDLVKF	IKLIHQAGLF	VHLRIGPFAC	AEWNFGGFV
asparagus	81	GHEPSPGQYY	FGGRYDLVRF	LKLVKQAGLY	AHLRIGPYVC	AEWNFGGFV
broccoli	81	AHEPSRRQYD	FSGNLDLVRF	IKTIQSAGLY	SVLRIGPYVC	AEWNYGGFP
Lupin	89	GHEPSPGKYY	FEDRFDLVGF	IKLVQQAGLF	VHLRIGPFIC	AEWNFGGFV

FIG. 3A

		160	170	180	190	200	
TBG1-ORF	127	WLKYVPGISF	RTNNEPFKAA	MQKFTTKIVD	MMK-----AE	KLYETQGGPI	176
TBG2-ORF	137	WLRDIPGIEF	RTDNAPFKEE	MERYVKKIVD	LMI-----SE	SLFSWQGGPI	186
TBG3-ORF	131	WLKYVPGISF	RTDNGPFKAA	MQKFTAKIVN	MMK-----AE	RLYETQGGPI	180
TBG4-ORF	129	WLKYVPGMEF	RTNNQPFKVA	MQGFVQKIVN	MMK-----SE	NLFESQGGPI	178
TBG5-ORF	151	WLHFIPGIEF	RTDNEPFKAE	MKRFTAKIVD	MIK-----QE	NLYASQGGPV	200
TBG6-ORF	151	WLKYVPGISF	RADNEPFKNA	MKGYAEKIVN	LMKIIIFSSL	RVVQSYSHRL	200
TBG7-ORF	150	WLHYVPGTTF	RTDSEPFKYH	MQKFMTYTVN	LMK-----RE	RLFASQGGPI	199
apple	130	WLKYVPGIAF	RTDNEPFKAA	MQKFTEKIVS	MMK-----AE	KLFQTQGGPI	179
carnation	135	WLKYVPGIEF	RTDNGPFKEK	MQVFTTKIVD	MMK-----AE	KLFHWQGGPI	184
asparagus	131	WLKYVPGIHF	RTDNGPFKAA	MGKFTEKIVS	MMK-----AE	GLYETQGGPI	180
broccoli	131	WLHNMPDMKF	RTINPGFMNE	MQNFTTKIVN	MMK-----EE	SLFASQGGPI	180
Lupin	139	WLKYVPGIAF	RTDNEPFKEA	MQKFTEKIVN	IMK-----AE	KLFQSQGGPI	188
		210	220	230	240	250	
TBG1-ORF	177	ILSQ-IENEY	GP--MEWELG	EPKKVYSEWA	AKMAVDLGTG	VPWI MCKQD-	226
TBG2-ORF	187	ILLQ-IENEY	GN--VESSFG	PKGKLYMKWA	AEMAVGLGAG	VPWVMCRQ-T	236
TBG3-ORF	181	ILSQ-IENEY	GP--MEWELG	APGKSYAQWA	AKMAVGLDTG	VPWVMCKQD-	230
TBG4-ORF	179	IMAQ-IENEY	GP--VEWEIG	APGKAYTKWA	AQMAVGLKTG	VPWI MCKQE-	228
TBG5-ORF	201	ILSQ-IENEY	GNGDIRESRYG	PRAKPYVNWA	ASMATSINTG	VPWVMCQQ-P	250
TBG6-ORF	201	RMSMGLKPRY	----LEHRDI	SIQHGLQIWQ	----LDLNTG	VPWVMCKEE-	250
TBG7-ORF	200	ILSQ-VENEY	G--YYENAYG	EGGKRYALWA	AKMALSQNTG	VPWI MC-QQY	249
apple	180	ILSQ-IENEY	GP--VEWEIG	APGKAYTKWA	AQMAVGLDTG	VPWI MCKQE-	229
carnation	185	ILNQ-IENEY	GP--VEWEIG	APGKAYTHWA	AQMAQSLNAG	VPWI MCKQDS	234
asparagus	181	ILSQ-IENEY	GP--VEYYDG	AAGKSYTNW	AKMAVGLNTG	VPWVMCKQD-	230
broccoli	181	ILAQ-IENEY	GN--VISSYG	AEGKAYIDWC	ANMANSLDIG	VPWI MC-QQP	230
Lupin	189	ILSQ-IENEY	GP--VEWEIG	APGKAYTKWA	AQMAVGLDTG	VPWVMCKQE-	238
		260	270	280	290	300	
TBG1-ORF	227	DVPDPPIINTC	NGFYCDYFTP	NKANKPKMWT	EAWTAWFTEF	GGPV PYRPAE	276
TBG2-ORF	237	DAPEYIIDTC	NAYYCDGFTP	NSEKKPKIWT	ENWNGWFADW	GERLPYRPSE	286
TBG3-ORF	231	DADPPIINAC	NGFYCDYFSP	NKAYKPKIWT	EAWTAWFTGF	GNPV PYRPAE	280
TBG4-ORF	229	DADPVIDTC	NGFYCEGFRP	NKPYKPKMWT	EVWTGWYTF	GGPIPQRPAE	278
TBG5-ORF	251	DAPPSVINTC	NGFYCDQFKQ	NSDKTPKMWT	ENWTGWFLSF	GGPV PYRPVE	300
TBG6-ORF	251	DADPPVINTC	NGFYCDNFFP	NKPYKPATWT	EAWSGWFS	GGPLHQRPVQ	300
TBG7-ORF	250	DADPVIDTC	NSFYCDQFKP	ISPINKPKIWT	ENWPWGFKTF	GARDPHRPAE	299
apple	230	DADPVIDTC	NGFYCENFKP	NKDYKPKMWT	EVWTGWYTEF	GGAVPTRPAE	279
carnation	235	DVPDNVIDTC	NGFYCEGFVP	KDKSKPKMWT	ENWTGWYTEY	GKPV PYRPAE	284
asparagus	231	DADPVINTC	NGFYCDYFSP	NKDNKPKMWT	EAWTGWFTGF	GGAVPQRPAE	280
broccoli	231	HAPQPMIETC	NGFYCDQYKP	SNPSSPKMWT	ENWTGWFKNW	GGKHPYRTAE	280
Lupin	239	DADPPIIDTC	NGFYCENFTP	NKNYKPKLWT	ENWTGWYTA	GGATPYRPAE	288

FIG. 3B

		310	320	330	340	350
TBG1-ORF	277	DMAFAVARFI	QTGGSFINYY	MYHGGTNFGR	TSGGPFIAATS	YDYDAPLDEF
TBG2-ORF	287	DI AFAI ARFF	QRGGSLQNYY	MYFGGTNFGR	TAGGPTQITS	YDYDAPLDEY
TBG3-ORF	281	DLAFSVAKFI	QKGGSFINYY	MYHGGTNFGR	TAGGPFIAATS	YDYDAPLDEY
TBG4-ORF	279	DI AFSVARFV	QNNGSFFNYY	MYHGGTNFGR	TSSGLFIATS	YDYDAPLDEY
TBG5-ORF	301	DI AFAVARFF	QRGGTFQNYY	MYHGGTNFGR	TSGGPFIAATS	YDYDAPLDEY
TBG6-ORF	301	DLAFAVAQFI	QRGGSFVNYY	MYHGGTNFGR	TAGGPFITTS	YDYDAPLDEY
TBG7-ORF	300	DVAYSVARFF	QKGGSVQNYY	MYHGGTNFGR	TAGGPFITTS	YDYDAPIDEY
apple	280	DVAFSVARFI	QSGGSFLNYY	MYHGGTNFGR	TAGGPFMATS	YDYDAPLDEY
carnation	285	DVAFSVARFI	QNNGSFMNYY	MFHGGTNFE-	TTAGRFVSTS	YDYDAPLDEY
asparagus	281	DMAFAVARFI	QKGGSFINYY	MYHGGTNFGR	TAGGPFISTS	YDYDAPIDEY
broccoli	281	DLAFSVARFF	QTGGTFQNYY	MYHGGTNFGR	VAGGPFITTS	YDYDAPLDEY
Lupin	289	DIAFSVARFI	QNRGSLFNYY	MYHGGTNFGR	TSNGLFVATS	YDYDAPIDEY
		360	370	380	390	400
TBG1-ORF	327	GSLRQPWKWH	LKDLHRAIKL	CEPALVSVD-	PTVTSLGNYQ	EARVFKSES-
TBG2-ORF	337	GLLRQPWKWH	LKDLHAAIKL	CEPALVAADS	PQYIKLGPKQ	EAHVYRGTSN
TBG3-ORF	331	GLLRQPWKWH	LKDLHRAIKL	CEPALVSGD-	PAVTALGHQQ	EAHVFRSKA-
TBG4-ORF	329	GLLNEPKYGH	LRDLHKAIKL	SEPALVSSY-	AAVTSLGNSQ	EAHVYRSKS-
TBG5-ORF	351	-----	-----	-----	-----	400
TBG6-ORF	351	-----	-----	-----	-----	400
TBG7-ORF	350	GLPRFPWKWH	LKELHKVIKS	CEHALLNND-	PTLLSLGPLQ	EADVYEDAS-
apple	330	GLPREPKWGH	LRDLHKAIKS	CESALVSVD-	PSVTKLGSNQ	EAHVFKSES-
carnation	335	GLPREPKYTH	LKNLHKAIKM	CEPALVSSD-	AKVTNLGSNQ	EAHVYSSNS-
asparagus	331	GLLRQPWKWH	LRDLHKAIKL	CEPALVSGE-	PTITSLGQNZ	ESYVYRSKS-
broccoli	331	GNLNQPWKWH	LKQLHTLLKS	MEKPLTYGNI	STID-LGNSV	TATVYSTNEK
Lupin	339	GLLNEPKWGH	LRELHRAIKQ	CESALVSVD-	PTVSWPGKNL	EVHLYKTES-
		410	420	430	440	450
TBG1-ORF	377	-----	GACAAFLANY	NQHSFAKVAF	GNMHYNLPPW	SISILPDCKN
TBG2-ORF	387	NIGQYMSLNE	GICAAFIANI	DEHESATVKF	YGQEFTLPPW	SVVF---CQI
TBG3-ORF	381	-----	GSCAAFLANY	DQHSFATVSF	ANRHYNLPPW	SISILPDCKN
TBG4-ORF	379	-----	GACAAFLSNY	DSRYSVKVTF	QNRPYNLPPW	SISILPDCKT
TBG5-ORF	401	-----	-----	-----	-----	450
TBG6-ORF	401	-----	-----	-----	-----	450
TBG7-ORF	400	-----	GACAAFLANM	DDKNDKVQF	RHVSYHLPW	SVSILPDCKN
apple	380	-----	D-CAAFLANY	DAKYSVKVF	GGGQYDLPPW	SISILPDCKT
carnation	385	-----	GSCAAFLANY	DPKWSVKVTF	SGMEFELPAW	SISILPDCKK
asparagus	381	-----	-SCAAFLANF	NSRYYATVTF	NGMHYNLPPW	SVSILPDCKT
broccoli	381	S-----	-SC--FIGNV	NATADALVNF	KGKDYNVPW	SVSILPDCDK
Lupin	389	-----	A-CAAFLANY	NTDYSTQVKF	GNGQYDLPPW	SISILPDCKT

FIG. 3C

		460	470	480	490	500	
TBG1-ORF	427	TVYNTARVGA	QSAQM--K--	-----	MTP	VSRGFS--WE	476
TBG2-ORF	437	AEIQLSTQLR	WGHKLQSKQW	AQILFQLGII	LCFYKLSLKA	SSESFSQSWM	486
TBG3-ORF	431	TVFNTARIGA	QSAQM--K--	-----	MTP	VSRGLP--WQ	480
TBG4-ORF	429	AVYNTAQVNS	QSSSI--K--	-----	MTP	AGGGGLS--WQ	478
TBG5-ORF	451	-----	-----	-----	-----	-----	500
TBG6-ORF	451	-----	-----	-----	-----	-----	500
TBG7-ORF	450	VAFNTAKVGC	QTTSIVNMAP-	-----ID	L--HPTASSP	KRDIKSLQWE	499
apple	430	EVYNTAKVGS	QSSQV--Q--	-----	MTP	VHSGF--WQ	479
carnation	435	EVYNTARVNE	PSPKLHSK--	-----	MTP	VISNLN--WQ	484
asparagus	431	TVFNTARVGA	QTTTM--K--	-----	MQY	LG-GFS--WK	480
broccoli	431	EAYNTARVNT	QTSSIITEDS-	-----C-----D	EPEKLKWTWR	480	
Lupin	439	EVFNTAKVNS	PRLHR--K--	-----	MTP	VNSAFA--WQ	488
		510	520	530	540	550	
TBG1-ORF	477	S-FNEDAASH	EDD-TFTVVG	LLEQINITRD	VSDYLWYMTD	IEIDPTE-GF	526
TBG2-ORF	487	T-LKEPLGVW	GDKN-FTSKG	I LEHLNVTKD	QSDYLWYLTR	IYISDDDISF	536
TBG3-ORF	481	S-FNEETSSY	EDS-SFTVVG	LLEQINTTRD	VSDYLWYSTD	VKIDSRE-KF	530
TBG4-ORF	479	S-YNEETPTA	DDSDTLTANG	LWEQKNVTRD	SSDYLWYMTN	VNIASNE-GF	528
TBG5-ORF	501	-----	-----	-----	-----	-----	550
TBG6-ORF	501	-----	-----	-----	-----	-----	550
TBG7-ORF	500	V-FKETAGVW	GVAD-FTKNG	FVDHINTTKD	ATDYLWYTT	IFVHAEE-DF	549
apple	480	S-FIEETTSS	DETDTTLDG	LYEQINITRD	TTDYLWYMTD	ITIGSDE-AF	529
carnation	485	S-YSDEVPTA	DSPGTREKK	LYEQINMTWD	KSDYLWYMTD	VVLDGNE-GF	534
asparagus	481	A-YTEDTDAL	NDN-TFTKDG	LVEQLSTTW	RSDYLWYTTY	VDIAKNE-EF	530
broccoli	481	PEFTTQKTIL	KGSGDLIAKG	LVDQKDVTND	ASDYLWYMTR	VHLDKKDPIW	530
Lupin	489	S-YNEEPASS	SENDPVGTGYA	LWEQVGVT	SSDYLWYLT	VNIGPND---	538
		560	570	580	590	600	
TBG1-ORF	527	LNSGN-WPWL	TVFSAGHALH	VVFVNGQLAGT	VYGSLENPKL	TFSNGINLRA	576
TBG2-ORF	537	WEENDVSPTI	DIDSMRDFVR	IFVNGQLAGS	VKGKW---I	KVVQPVKLVQ	586
TBG3-ORF	531	LRGGK-WPWL	TIMSAGHALH	VVFVNGQLAGT	AYGSLEKP	TF SKAVNLRA	580
TBG4-ORF	529	LKNKGK-DPYL	TVMSAGHVLH	VVFVNGKLSGT	VYGTLDNP	TYSGNVKLRA	578
TBG5-ORF	551	-----	-----	-----	-----	-----	600
TBG6-ORF	551	-----	-----	-----	-----	-----	600
TBG7-ORF	550	LRN-RGTAML	FVESKGHAMH	VFINKKLQAS	ASGNGTVPQF	KFGTPIALK	599
apple	530	LKNKGK-SPLL	TIFSAGHALN	VFIINGQLSGT	VYGSLENPKL	SFSQNVNLRS	579
carnation	535	LKKGD-EPWL	TVNSAGHVLH	VVFVNGQLQGH	AYGSLAKPQL	TF SQKV	584
asparagus	531	LKTGK-YPYL	TVMSAGHAVH	VFIINGQLSGT	AYGSLDNPKL	TYSGSAKLWA	580
broccoli	531	SRNMS----L	RVHSNAHVLH	AYVNGKYVGN	QIVRDNKFDY	RFEKKVNLVH	580
Lupin	539	IKDGK-WPVL	TAMSAGHVLN	VFIINGQYAGT	AYGSLDDPRL	TF SQSVNL	588

FIG. 3D

		610	620	630	640	650
TBG1-ORF	577	GVNKISLLSI	AVGLPNVGPH	FETWNAGVLG	PVSLNGLNEG	T---RDLTWQ
TBG2-ORF	587	GYNDILLSE	TVGLQNYGAF	LEKDAGFKG	QIKLTGCKSG	D---INLTTS
TBG3-ORF	581	GVNKISLLSI	AVGLPNIGPH	FETWNAGVLG	PVSLTGLDEG	K---RDLTWQ
TBG4-ORF	579	GINKISLLSV	SVGLPNVGVH	YDTWNAGVLG	PVTLSGLNEG	S---RNLAQK
TBG5-ORF	601	-----	-----	-----	-----	650
TBG6-ORF	601	-----	-----	-----	-----	650
TBG7-ORF	600	GKNEISLLSM	TVGLQTAGAF	YE-WIGAGPT	SVKVAGFKTG	T---MDLTAS
apple	580	GINKLALLSI	SVGLPNVGTH	FETWNAGVLG	PITLKGLNSG	T---WDMGW
carnation	585	GVNRISLLSA	VVGLANVGWH	FERYNQGVLG	PVTLSGLNEG	T---RDLTWQ
asparagus	581	GSNKISILSV	SVGLPNVGNH	FETWNTGVLG	PVTLTGLNEG	K---RDLSLQ
broccoli	581	GTNHLALLSV	SVGLQNYGPF	FESGPTGING	PVKLVGYKGD	ETIEKDLSKH
Lupin	589	GNNKISLLSV	SVGLANVGTH	FETWNTGVLG	PVTLTGLSSG	T---WDLSKQ
		660	670	680	690	700
TBG1-ORF	627	KWFYKVGLKG	EALSLHSLSG	SPSVE--WVE	GSLVAQKQPL	SWYKTTFNAP
TBG2-ORF	637	LWTYQVGLRG	EFLEVYDVNS	TESAG--WTE	FPTGTPSVE	SWYKTKFDAP
TBG3-ORF	631	KWSYKVGLKG	EALSLHSLSG	SSSVE--WVE	GSLVAQRQPL	TWYKSTFNAP
TBG4-ORF	629	KWSYKVGLKG	ESLSLHSLSG	SSSVE--WVR	GSLMAQKQPL	TWYKATFNAP
TBG5-ORF	651	-----	-----	-----	-----	700
TBG6-ORF	651	-----	-----	-----	-----	700
TBG7-ORF	650	AWTYKIGLQG	EHLRIQKSYN	LKSKI--WAP	TSQPPKQQPL	TWYKAVVDAP
apple	630	KWTYKTGLKG	EALGLHTVTG	SSSVE--WVE	GPSMAEKQPL	TWYKATFNAP
carnation	635	YWSYKIGTKG	EEQQVYNNSGG	SSHVQ--WGP	PAW---KQPL	VWYKTTFDAP
asparagus	631	KWTYQIGLHG	ETLSLHSLTG	SSNVE--WGE	AS---QKQPL	TWYKTFFNAP
broccoli	631	QWDYKIGLNG	FNHKLFSMKS	AGHHHRKWST	EKLPADRM-L	SWYKANFKAP
Lupin	639	KWSYKIGLKG	ESLSLHTEAG	SNSVE--WVQ	GSLVAKKQPL	AWYKTTFSAP
		710	720	730	740	750
TBG1-ORF	677	DGNEPLALDM	NTMGKGQVWI	NGQSLGRHWP	AYKSS-GSCS	V-CNYTGWFD
TBG2-ORF	687	GGTDPVALDF	SSMGKGQAWV	NGHHVGRYWT	LVAPN-NGCG	RTCDYRGAYH
TBG3-ORF	681	AGNDPLALDL	NTMGKGQVWI	NGQSLGRYWP	GYKAS-GNCG	A-CNYAGWFN
TBG4-ORF	679	GGNDPLALDM	ASMGKGQIWI	NGEGVGRHWP	GYIAQ-GDCS	K-CSYAGTFN
TBG5-ORF	701	-----	-----	-----	-----	750
TBG6-ORF	701	-----	-----	-----	-----	750
TBG7-ORF	700	PGNEPVALDM	IHMKGKMAWL	NGQEIGRYWP	RRTSKYENCV	TQCDYRGKFN
apple	680	PGDAPLALDM	GSMGKGQIWI	NGQS VGRHWP	GYIAR-GSCG	D-CSYAGTYD
carnation	685	GGNDPLALDL	GSMGKGQAWI	NGQSIGRHWS	NNIAK-GSCN	DNCNYAGTYT
asparagus	681	PGNEPLALDM	NTMGKGQIWI	NGQSIGRYWP	AYKAS-GSCG	S-CDYRGTYN
broccoli	681	LGKDPVI VDL	NGLGKGEVWI	NGQSIGRYWP	SFNSSDEGCT	EEDDYRGEYG
Lupin	689	AGNDPLALDL	GSMGKGEVWV	NGQSIGRHWP	GNKAR-GNCG	N-CNYAGTYT

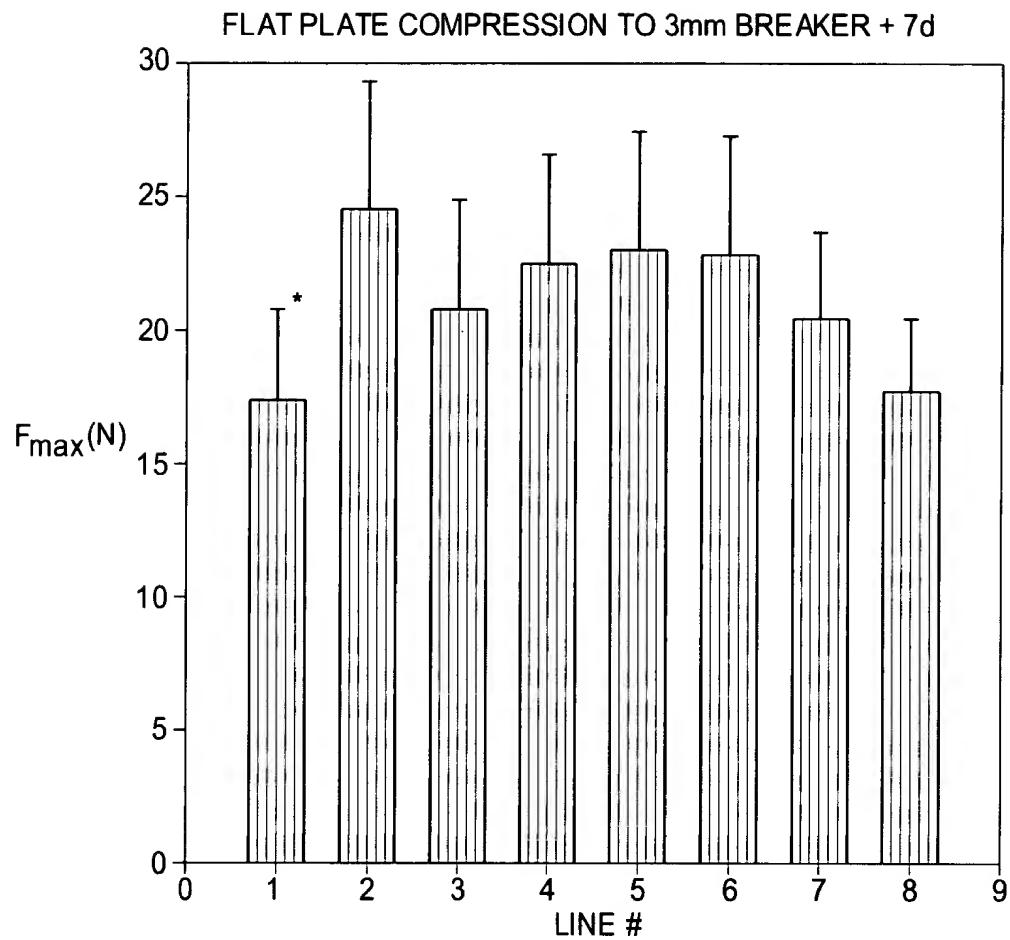
FIG. 3E

		760	770	780	790	800
TBG1-ORF	727	EKKCLTNCGE	GSQRWYHVPR	SWLYPTGNLL	V-VFEEWGGD	PYGITLVKRE
TBG2-ORF	737	SDKCRTNCGE	ITQAWYHIPR	SWLKTLNNVL	V-IFEETDKT	PFDISISTRS
TBG3-ORF	731	EKKCLSNCGE	ASQRWYHVPR	SWLYPTGNLL	V-LFEEWGGE	PHGISLVKRE
TBG4-ORF	729	EKKCQTNCGQ	PSQRWYHVPR	SWLKPSGNLL	V-VFEEWGGN	PTGISLVRRS
TBG5-ORF	751	-----	-----	-----	-----	800
TBG6-ORF	751	-----	-----	-----	-----	800
TBG7-ORF	750	PDKCVTGCQ	PTQRWYHVPR	SWFKPSGNVL	I-IFEEIGGD	PSQIRFSMRK
apple	730	DKKCRTHCGE	PSQRWYHI PR	SWLPTGNLL	V-VFEEWGGD	PSRISLVERG
carnation	735	ETKCLSDCGK	SSQKWYHVPR	SWLQPRGNLL	V-VFEEWGGD	TKWVSLVKRT
asparagus	731	EKKCLSNCGE	ASQRWYHVPR	SWLIPTGNFL	V-VLEEWGGD	PTGISMVKRS
broccoli	731	SDKCAFMC GK	PTQRWYHVPR	SFLNDKGHN T	ITLFEEEMGGD	PSMVKFKTVV
Lupin	739	DTKCLANCGQ	PSQRWYHVPR	SWLRSGGNYL	V-VLEEWGGD	PNGIALVERT
		810	820	830	840	850
TBG1-ORF	777	IGSVCADIYE	WQ-PQLLNWQ	RLVSGKFDRP	LR--PKAHLK	CAPGQKISSI
TBG2-ORF	787	TETICAQVSE	KHYPPLHKWS	HSEFDRKL SL	MDKTPEMHLQ	CDEGHTISSI
TBG3-ORF	781	VASVCADINE	WQ-PQLVNWQ	MQASGKVDPK	LR--PKAHL S	CASGQKITSI
TBG4-ORF	779	-----	-----	-----	R-	-----
TBG5-ORF	801	-----	-----	-----	-----	828
TBG6-ORF	801	-----	-----	-----	-----	850
TBG7-ORF	800	VSGACGHLSV	-DHPSFD--V	ENLOGSEIEN	DKNRPTLSLK	CPTNTNISSV
apple	780	-----	-----	-----	TA LD--AK	-----
carnation	785	IA-----	-----	-----	-----	829
asparagus	781	VASVCAEV E	LQ-PTMDNWR	TKAYG-----	R--PKVHLS	CDPGQKMSKI
broccoli	781	TGRVCAKAHE	-----	-----	HNKVELS	CN-NRPISAV
Lupin	789	-----	-----	-----	-----	830
		860	870	880	890	900
TBG1-ORF	827	KFASF GTPEG	VCGNFQQGSC	HAPRSYDAFK	K----NCVG	KESCSVQVTP
TBG2-ORF	837	EFASYGSPNG	SCQKFSQGKC	HAANSLSV--	--VSQACIG	RTSCSIGISN
TBG3-ORF	831	KFASF GTPQG	VCGSFREGSC	HAFHSYDAFE	R----YCIG	QNSCSVPVTP
TBG4-ORF	829	-----	-----	-----	-----	878
TBG5-ORF	851	-----	-----	-----	-----	900
TBG6-ORF	851	-----	-----	-----	-----	900
TBG7-ORF	850	KFASF GNPN	TCGSYMLGDC	HDQNSAALVE	K----VCLN	QNECALEMSS
apple	830	-----	-----	-----	-----	879
carnation	835	-----	-----	-----	-----	884
asparagus	831	KFASF GTPQG	TCGSFSEGSC	HAHKSYDAFE	QEGLMQNCVG	QEFC SVNVAP
broccoli	831	KFASF GNP SG	QCGSFAAGSC	EGAKDAVKV-	---VAKECVG	KLNCTMN VSS
Lupin	839	-----	-----	-----	-----	880

FIG. 3F

		910	920	930	940	950
TBG1-ORF	877	ENFGGDP-CR	NVLKKLSVEA	ICS-----
TBG2-ORF	887	GVFG-DP-CR	HVVKSLAVQA	KCSPPPDLST	SASS.....
TBG3-ORF	881	EIFGGDP-CP	HVMKKLSVEV	ICS-----
TBG4-ORF	879	-----	-----	-----
TBG5-ORF	901	-----	-----	-----
TBG6-ORF	901	-----	-----	-----
TBG7-ORF	900	ANFNMQI-CP	STVKKLAVEV	NCS-----
apple	880	-----	-----	KL-----
carnation	885	-----	-----	-----
asparagus	881	EVFGGDP-CP	GTMKKLAVEA	ICE-----
broccoli	881	HKFGSNLDCG	DSPKRLFVEV	EC-----

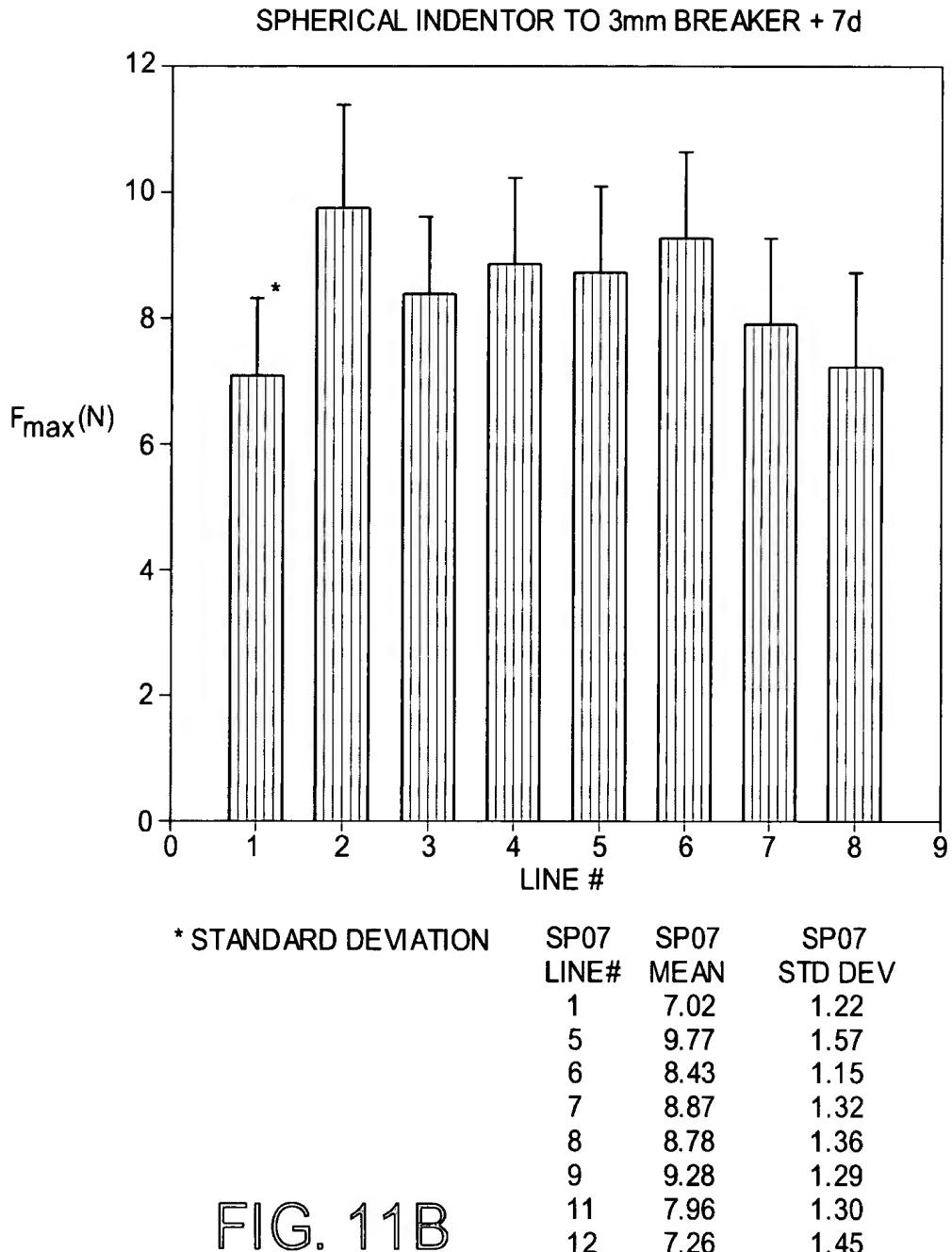
FIG. 3G

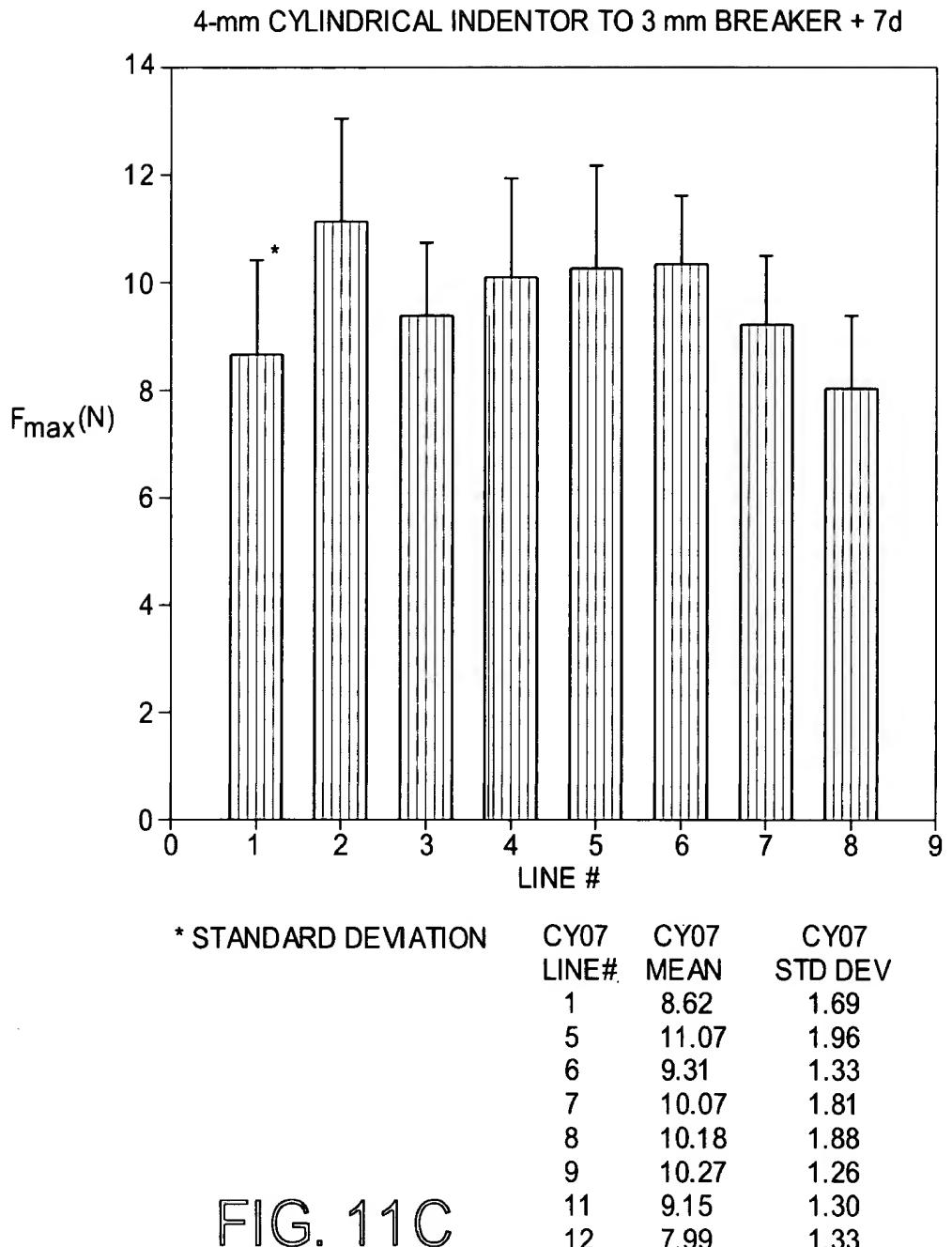


* STANDARD DEVIATION

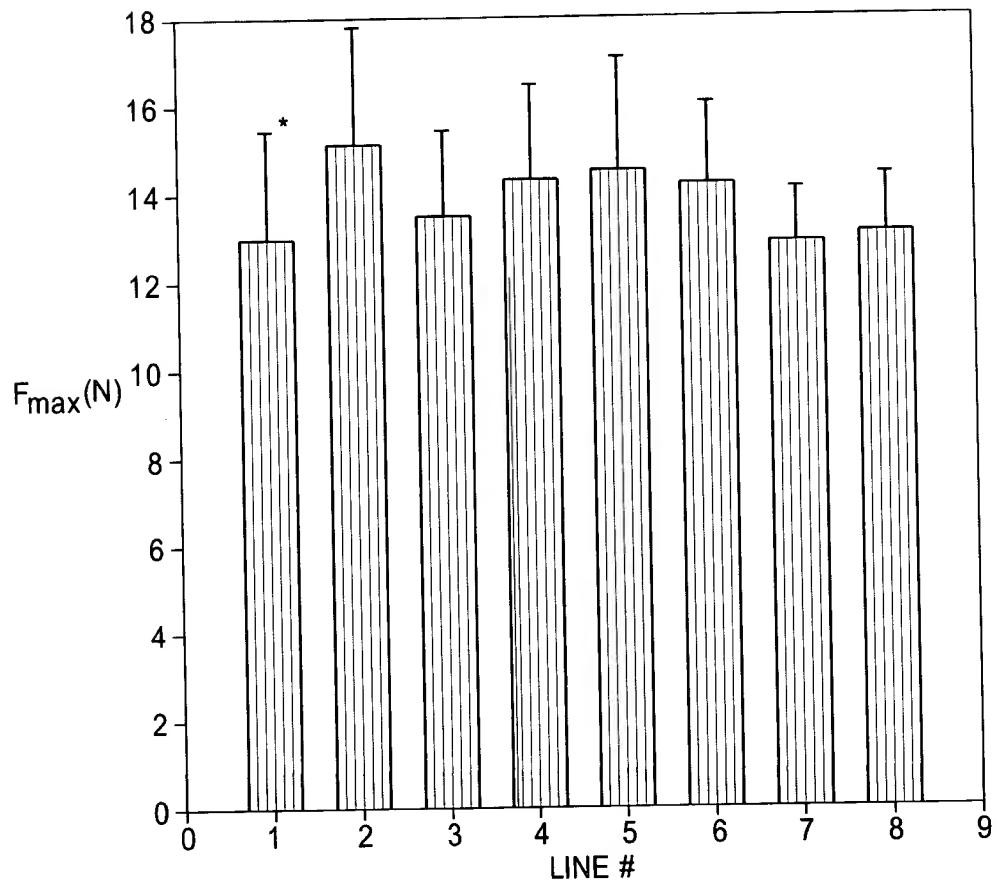
LINE#	FP07 MEAN	FP07 STD DEV
1	17.52665	3.418542
2	24.56026	4.786548
3	20.81681	4.066194
4	22.54655	4.15923
5	23.03255	4.493091
6	22.84338	4.517462
7	20.36124	3.24608
8	17.81924	2.665468

FIG. 11A





4-mm CYLINDRICAL PUNCTURE TO 10mm BREAKER + 7d



* STANDARD DEVIATION	PU07 LINE#	PU07 MEAN	PU07 STD DEV
	1	12.91	2.43
	5	15.13	2.61
	6	13.44	1.90
	7	14.28	2.16
	8	14.47	2.58
	9	14.14	1.81
	11	12.90	1.20
	12	13.18	1.25

FIG. 11D

FLAT PLATE COMPRESSION TO 3mm
BREAKER + 7d

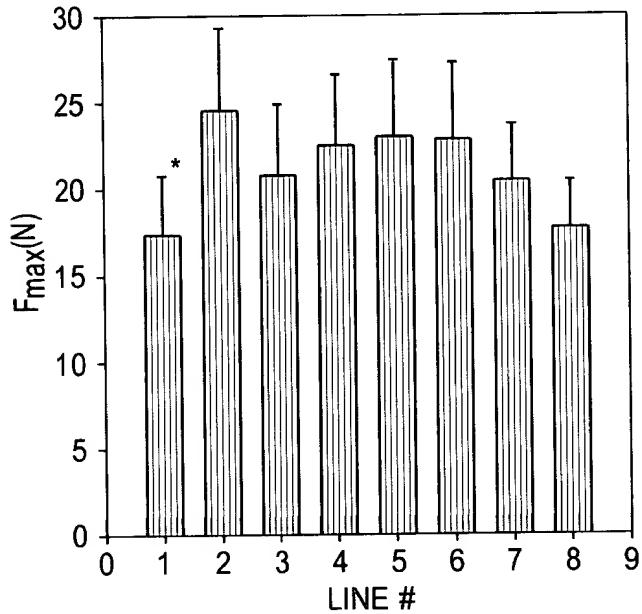


FIG. 11E(1)

SPHERICAL INDENTOR TO 3mm
BREAKER + 7d

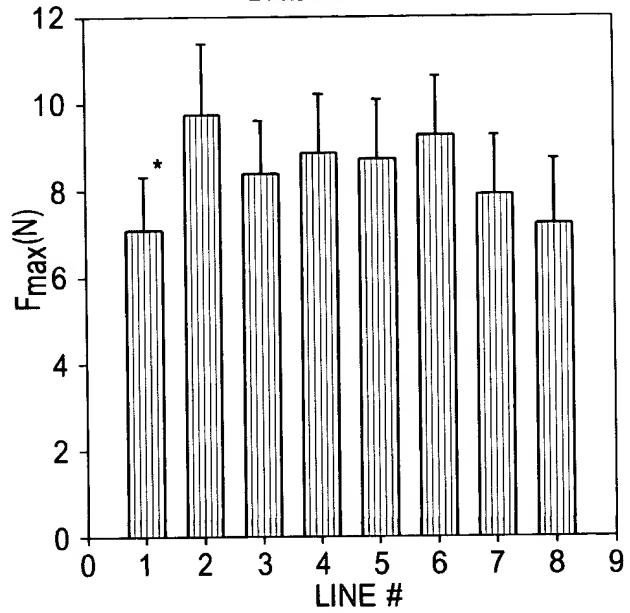


FIG. 11E(2)

4-mm CYLINDRICAL INDENTOR TO 3 mm
BREAKER + 7d

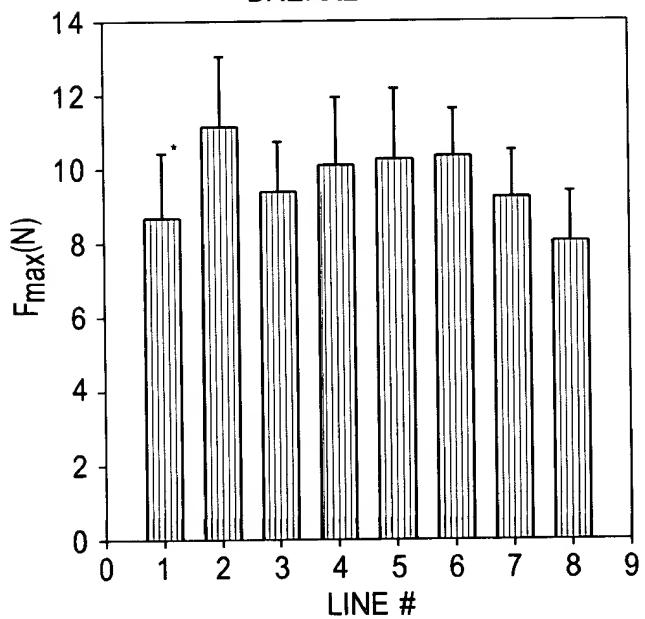


FIG. 11E(3)

4-mm CYLINDRICAL PUNCTURE TO 10 mm
BREAKER + 7d

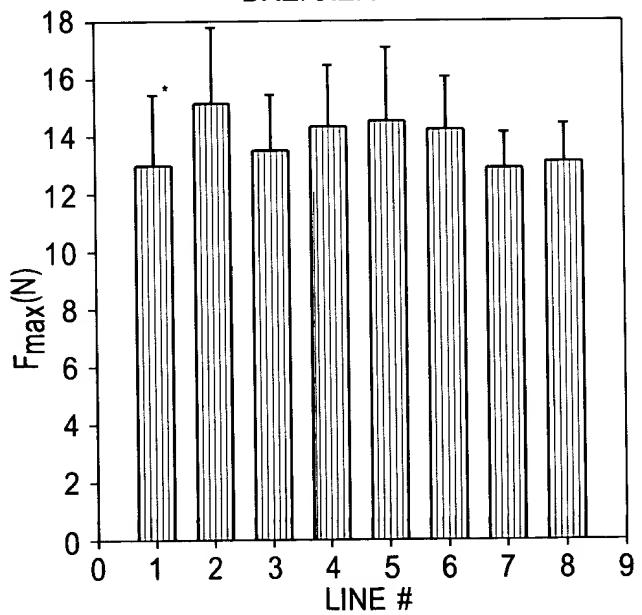


FIG. 11E(4)

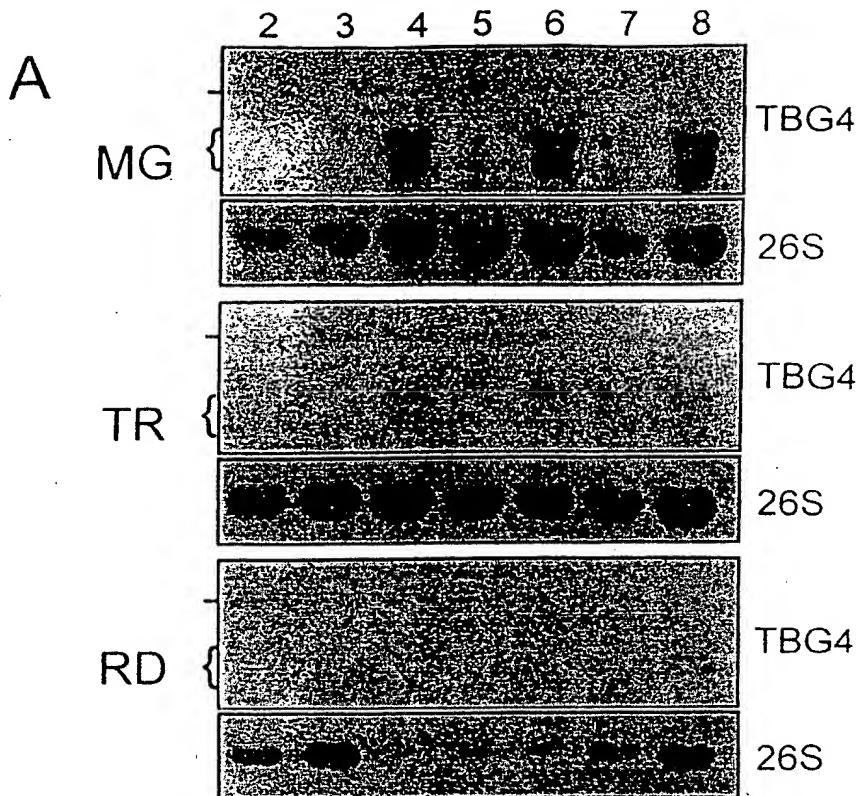


FIG. 12A

Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct. A. Total RNA was extracted from mature green/42 days post-pollination (MG), turning/breaker + 3 (TR) and red/breaker + 7 (RD) fruit and twenty μ g was loaded in each lane. RNAs were separated in an agarose gel and transferred to nylon membrane. Blots were hybridized using the probes indicated to the right, washed to a final stringency of 0.1X SSC at 65°C and were used to expose x-ray film. A 26S ribosomal gene clone from soybean was used as a loading control. The marks - and { denote the positions of the endogenous TBG4 and antisense mRNAs respectively. Lanes 2-8 correspond to transgenic lines 2-8 in Figures 11A-E.

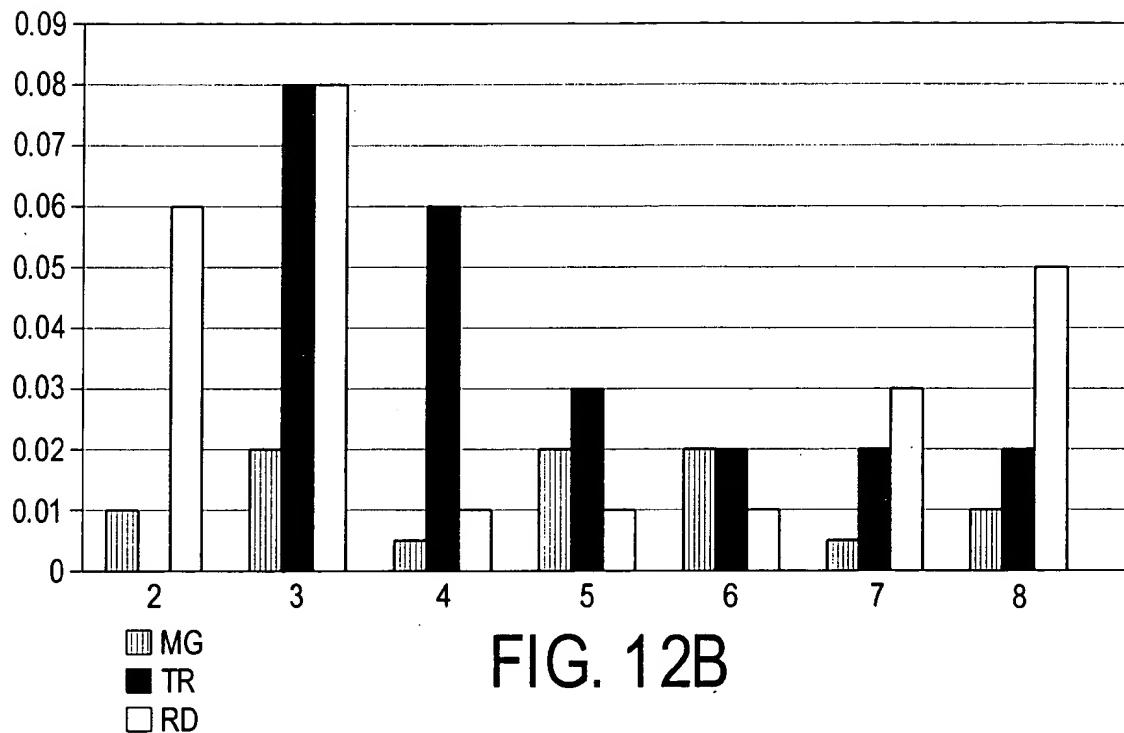


FIG. 12B

Figure 12. Northern blot analysis of TBG4 expression in transgenic fruit containing TBG4 antisense construct.

B. Chart of TBG4

mRNA levels in lines 2-8. Autoradiographs were scanned using a densitometer and TBG4 mRNA levels were corrected against the loading controls. TBG4 mRNA levels are shown in arbitrary units.

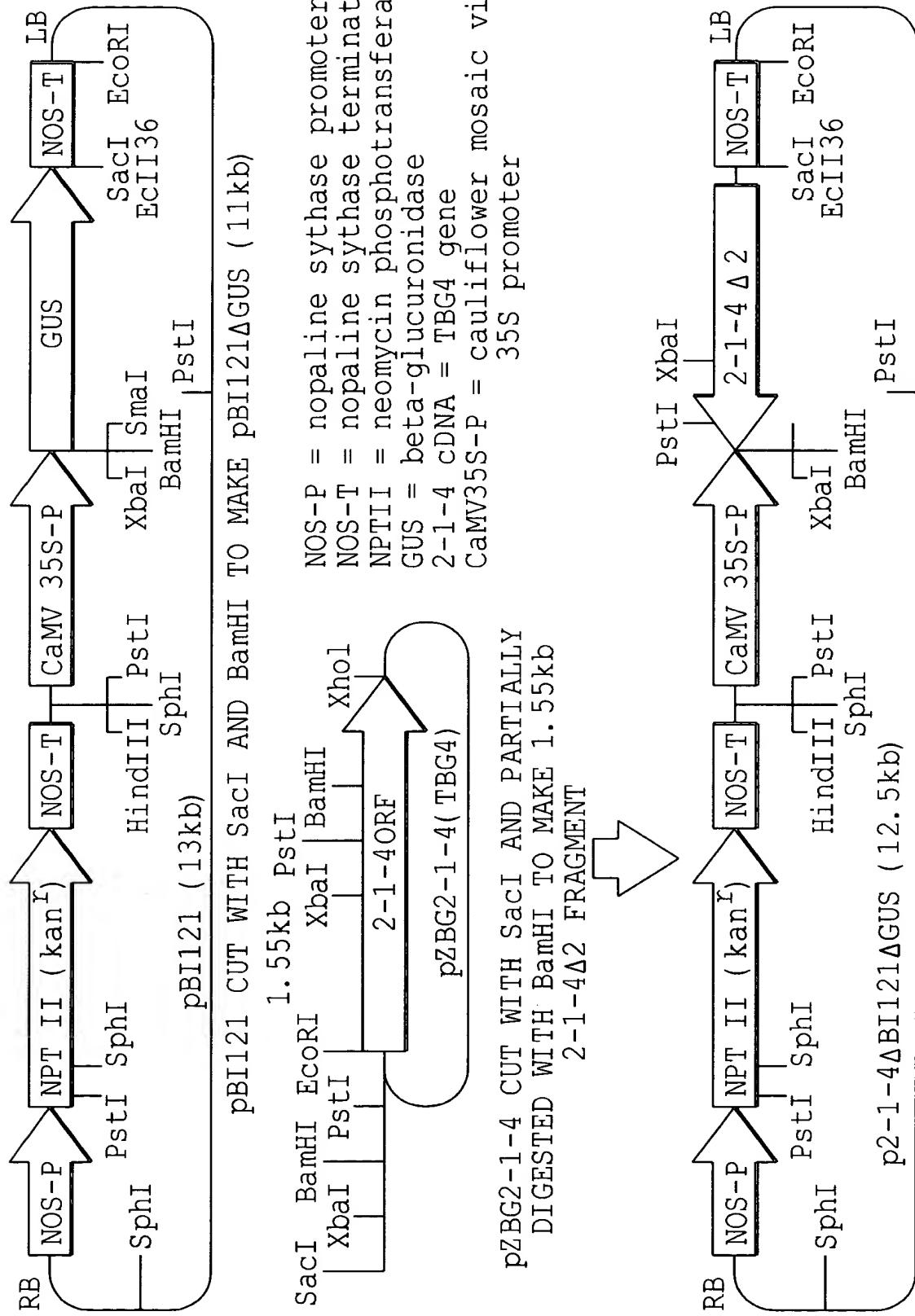
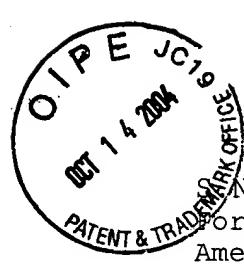


FIG. 13 BINARY CONSTRUCT USED TO TRANSFORM PLANTS AND EXPRESS TBG4
(pZBG2-1-4 IN THE ANTISENSE ORIENTATION)



N. 09/701,868

Formalized Drawings (45 sheets) (Figures 1,2,3,11,12 &13)
Amendment (37 CFR 1.312(a))

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* K. Gross et al. *
* (Name of applicant, assignee, or Registered Representative) *
* Colleen A. Dranecker 10-12-04 *
* (Signature) (Date) *
